

7b 155

14may03 11:19:38 User:208669 Session D2288.1

\$0.28 0.081 DialUnits File1

\$0.28 Estimated cost File1

\$0.28 Estimated cost this search

\$0.28 Estimated total session cost 0.081 DialUnits

File 155:MEDLINE(R) 1966-2003/May W1

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*File 155: Medline has been reloaded and accession numbers have changed. Please see HELP NEWS 155.

Set Items Description

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7 ds

Set Items Description

S1 19809 VIRUS AND (RECEPTOR OR RECEPTORS)

S2 930316 DT=REVIEW?

S3 2087 S1 AND S2

S4 11103 S1/T1

S5 702 S4 AND S3

S6 142 SEQUENCE? AND S5

S7 25362 CAR OR HCAR OR MCAR OR COXSACKIE OR ADENOVIRUS

S8 65 S3 AND S7

S9 0 VIRAL ADJ RECEPTOR?

S10 1384 VIRAL (W) RECEPTOR?

S11 160 S2 AND S10

S12 35 S10/T1

S13 294214 MUTATION OR MUTANT

S14 593482 RECEPTOR OR RECEPTORS

S15 9325 S13 (3N)S14

S16 463 S1 AND S15

S17 24 S2 AND S16

S18 4860 S13 (N)S14

S19 232 S18 AND S1

71s67/13

6/7/13

DIALOG(R)File 155:MEDLINE(R)

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11640582 99074492 PMID: 9852300

CD46 (membrane cofactor protein of complement, measles virus receptor); structural and functional divergence among species (review).

Seya T, Nomura M, Murakami Y, Begun N A, Matsumoto M, Nagasawa S
Department of Immunology, Osaka Medical Center for Cancer and
Cardiovascular Diseases, Higashinari-ku, Osaka 537, Japan.

International journal of molecular medicine (GREECE) May 1998, 1 (5)
p809-16, ISSN 1107-3756 Journal Code: 9810955

Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Human CD46 was identified as a complement regulator and was later shown to be a measles virus receptor. The ubiquitous distribution profile of CD46 accounted for systemic measles infection and general protection of host tissue/organs from autologous complement. A similar ubiquitous distribution was observed for swine and simian CD46 homologues based upon subsequent cDNA cloning and Northern analysis, reinforcing the roles of CD46. In contrast, recent cDNA cloning and distribution analyses of murine and guinea-pig CD46 revealed the predominant expression of these rodent CD46 homologues in the testis, especially in mature testicular germ cells. These results do not support the established functions of human CD46 but support the hypothesis that CD46 on sperm serves as a fertilization-related adhesion molecule toward eggs. Here, we review the structure, function and distribution of human CD46 and discuss the possible differences between human CD46 and its homologues recently cloned from a variety of non-human primates and other animals. (72 Refs.)

Record Date Created: 19990224

Record Date Completed: 19990224

71s87/2 20 26 47 53 54

8/7/2

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.

14742747 22514653 PMID: 12627395

Structural evidence for common functions and ancestry of the reovirus and adenovirus attachment proteins.

Stehle Thilo; Dermody Terence S

Laboratory of Developmental Immunology and Renal Unit, Massachusetts
General Hospital, Harvard Medical School, Boston, MA 02114, USA.
tstehle@partners.org

Reviews in medical virology (England) Mar-Apr 2003, 13 (2) p123-32,
ISSN 1052-9276 Journal Code: 9112448

Contract/Grant No.: AI38296; AI; NIAID; AI45716; AI; NIAID

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The crystal structure of the reovirus attachment protein, sigma1, reveals a fibre-like structure that is remarkably similar to that of the adenovirus attachment protein, fibre. Both proteins are trimers with head-and-tail morphology. They share unique domain structures and functional properties including defined regions of flexibility within the tail and an unusual symmetry mismatch with the pentameric viral capsid protein into which they are inserted. Moreover, the receptors for reoviruses and adenoviruses, junctional adhesion molecule 1 and coxsackievirus and adenovirus receptor, respectively, also share key structural and functional properties. Although reoviruses and adenoviruses belong to different virus families and have few

properties in common, the observed similarities between signal and fibre point to a conserved mechanism of attachment and an ancient evolutionary relationship. Copyright 2003 John Wiley & Sons, Ltd. (66 Refs.)

Record Date Created: 20030310

Record Date Completed: 20030425

8/7/20

DIALOG(R)File 155:MEDLINE(R)

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11427447 98309961 PMID: 9645993

Coxsackie B virus and its interaction with permissive host cells.

Selinka H C; Huber M; Pasch A; Klingel K; Aepinus C; Kandolf R

Department of Molecular Pathology, University of Tübingen, Germany.

hans-christoph.selinka@med.uni-tuebingen.de

Clinical and diagnostic virology (NETHERLANDS) Apr 1998, 9 (2-3)

p115-23, ISSN 0928-0197 Journal Code: 9309653

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

BACKGROUND: Observations in humans and the results of experiments on laboratory animals have provided evidence that coxsackieviruses of group B (CVB) are major etiologic agents of acute and chronic enterovirus myocarditis and various other virus-induced diseases. OBJECTIVE: This minireview briefly summarizes the investigations to elucidate various molecular mechanisms for the induction and maintenance of persistent CVB infections. With regard to the recent findings that CVB may use several different receptor proteins, this article focuses on virus-host cell interactions and the potential impact of these interactions for enteroviral replication. STUDY DESIGN: The interaction of CVB with specific cell surface proteins was analyzed in cultured cell lines and murine tissues at the level of virus attachment and virus internalization. As example for the interaction of CVB with intracellular proteins, the state of p21rasGTPase-activating protein (RasGAP) was investigated in mock-infected and CVB3-infected HeLa cells. RESULTS AND CONCLUSIONS: The experiments to elucidate the virus receptor interactions revealed the necessity to differentiate between CVB attachment proteins and proteins involved in virus internalization. Since more than one protein may be required to initiate the uptake of CVB into permissive host cells, a model of the putative interaction of these proteins within a multimeric receptor complex is proposed. It is further tempting to speculate that the presence of multiple attachment proteins may influence the tissue tropism of CVB as well as pathogenicity. (39 Refs.)

Record Date Created: 19980916

Record Date Completed: 19980916

8/7/26

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.

11085523 97440728 PMID: 9294931

Identification and biology of cellular receptors for the coxsackie B viruses group.

Kuhn R J

Department of Biological Sciences, Purdue University, West Lafayette, Indiana 47907, USA.

Current topics in microbiology and immunology (GERMANY) 1997, 223 p209-26, ISSN 0070-217X Journal Code: 0110513

Document type: Journal Article; Review; Review Literature

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

(65 Refs.)

Record Date Created: 19971022

Record Date Completed: 19971022

8/7/47

DIALOG(R)File 155:MEDLINE(R)

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09588865 21372597 PMID: 11479928

Receptor for the group B coxsackieviruses and adenoviruses: CAR.

Carson S D

Department of Pathology and Microbiology, University of Nebraska Medical Center, Omaha, NE 68198-6495, USA. scarson@unmc.edu

Reviews in medical virology (England) Jul-Aug 2001, 11 (4) p219-26, ISSN 1052-9276 Journal Code: 91112448

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Considerable progress towards the characterisation of the long-sought receptor, CAR (coxsackievirus and adenovirus receptor), shared by group B coxsackieviruses (CVB) and most adenoviruses (Ad) has been made since it was isolated and cloned in 1997. The primary sequence of CAR shows that it is a member of the immunoglobulin superfamily of proteins, containing two Ig superfamily domains: an amino-terminal V-like module and a C2-like module. The CAR cytoplasmic domain, representing nearly one-third of the protein, is separated from the C2-like module by a single membrane-spanning sequence. The structure of the CAR V-like module complexed with the Ad fibre knob has been determined using recombinant proteins, and reveals three CAR modules associated with a single knob. Although recombinant CAR expressed in mammalian cells confers permissivity to CVB infection, details of the interaction between CAR and CVB remain to be elucidated. The expression of CAR appears to be highly regulated with respect to both cell type and developmental age. In rodents, CAR is expressed at high levels

just before birth, and declines thereafter. Expressed levels have been found to increase in regenerating muscle and in response to immunological mediators or inflammation, and in RD cells and umbilical vein endothelial cells in response to high cell density. These studies indicate that CAR expression is highly regulated, but the mechanisms and molecules that mediate the expression remain to be discovered. The physiological function of CAR and its natural ligand also remain to be discovered. In addition, while CAR expression generally correlates with viral tropism, the relationship between the physiological function of CAR and the pathologies of CVB and Ad infections remain to be described. Copyright 2001 John Wiley & Sons, Ltd. (45 Refs.)

Record Date Created: 20010731
Record Date Completed: 20020404

8/7/53

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.
09098690 20396567 PMID: 10936081

Cell receptors involved in adenovirus entry.

Nemerow G R

Department of Immunology, Scripps Research Institute, La Jolla, California 92037, USA. gnemerow@scripps.edu

Virology (UNITED STATES) Aug 15 2000, 274 (1) p1-4, ISSN 0042-6822
Journal Code: 0110674

Contract/Grant No.: EY11431; EY; NEI; HL54352; HL; NHLBI

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

(18 Refs.)

Record Date Created: 20000925

Record Date Completed: 20000925

8/7/54

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.
09016780 20310108 PMID: 10851559

[Cell receptors for human adenoviruses]

Recepteurs cellulaires des adenovirus humains.

Boulangier P

Laboratoire de Virologie et Pathogenese Moleculaire, Faculte de Medecine de Montpellier, CNRS UMR 5812, Montpellier.

Journal de la Societe de biologie (FRANCE) 1999, 193 (1) p77-84,
Journal Code: 100890617

Document type: Journal Article; Review; Review, Tutorial ; English
Abstract

Languages: FRENCH

Main Citation Owner: NLM

Record type: Completed

During the early stage of the adenovirus infection, the virion binds to a "primary receptor" on the host cell plasma membrane via the fibre projection jutting out of the penton base capsomers located at the twelve apices of the icosahedral capsid. The second step consists of a receptor-mediated endocytosis which involves membrane integrin molecules (the "secondary receptors") and the RGD and/or LDV motifs of penton base. The latter step is inhibited at low temperature, whereas virus attachment to its primary receptor is temperature-independent. Two different primary receptors with a high affinity for the Adenovirus have been recently identified. One is common to Coxsackievirus B3 and adenovirus (CAR), the other one corresponds to a conserved region of the alpha-2 domain of the heavy chain of the major histocompatibility complex class I molecules (MHC-I-alpha 2), overlapping tryptophane-167. The receptor usage by the virus is governed by both cellular and viral parameters. On the cellular side, the relative abundance of one versus the other type of primary receptors would theoretically determine the virus choice: CAR receptor has been mainly found in tissues from mesodermic origin, whereas MHC-I-alpha 2 is ubiquitous. On the virus side, the molecular determinants of the receptor usage have been mapped to the terminal knob of the fiber projection, and have been found to be different for CAR and MHC-I-alpha 2. CAR recognizes linear motifs in fiber knobs in a subgroup-dependent manner, as it binds to all Adenovirus serotypes except for the subgroup B members. MHC-I-alpha 2 however recognizes conformational epitopes carried by fiber knobs from all serotypes tested including subgroup B members. These results should have significant implications in the cell targeting of adenoviral vectors used in gene therapy. (56 Refs.)

Record Date Created: 20000630
Record Date Completed: 20000630
? t s127/21 22
127/21

DIALOG(R)File 155:MEDLINE(R)

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07367084 92230251 PMID: 1566586

A single point mutation of the influenza C virus glycoprotein (FIEF) changes the viral receptor-binding activity.

Szepanski S; Gross H J; Brossmer R; Klenk H D; Hentler G
Institut für Virologie, Philipps-Universität Marburg, Germany.

Virology (UNITED STATES) May 1992, 188 (1) p85-92, ISSN 0042-6822
Journal Code: 0110674

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

From strain JHB/1/66 of influenza C virus a mutant was derived with a change in the cell tropism. The mutant was able to grow in a subline of

Madin-Darby canine kidney cells (MDCK II) which is resistant to infection by the parent virus due to a lack of receptors. Inactivation of cellular receptors by either neuraminidase or acetyltransferase and generation of receptors by resialylation of cells with N-acetyl-9-O-acetylneuraminic acid (Neu5,9Ac2) indicated that 9-O-acetylated sialic acid is a receptor determinant for both parent and mutant virus. However, the mutant required less Neu5,9Ac2 on the cell surface for virus attachment than the parent virus. The increased binding efficiency enabled the mutant to infect cells with a low content of 9-O-acetylated sialic acid which were resistant to the parent virus. By comparing the nucleotide sequences of the glycoprotein (HEF) genes of the parent and the mutant virus only a single point mutation could be identified on the mutant gene. This mutation at nucleotide position 872 causes an amino acid exchange from threonine to isoleucine at position 284 on the amino acid sequence. Sequence similarity with a stretch of amino acids involved in the receptor-binding pocket of the influenza A hemagglutinin suggests that the mutation site on the influenza C glycoprotein (HEF) is part of the receptor-binding site.

Record Date Created: 19920515
Record Date Completed: 19920515

12/7/22

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.
06152964 89168410 PMID: 2538240

Viral receptors of the immunoglobulin superfamily.

White J M; Litman D R

Department of Pharmacology, University of California, San Francisco 94143.

Cell (UNITED STATES) Mar 10 1989, 56 (5) p725-8, ISSN 0092-8674
Journal Code: 0413066

Document type: Journal Article; Review; Tutorial

Language: ENGLISH

Main Citation Owner: NLM

Record type: Completed

(18 Refs.)

Record Date Created: 19890425

Record Date Completed: 19890425
71s197/5

197/5

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.
14198605 22326847 PMID: 12438620

Mutations in the N-terminal domains of necrin-1 and necrin-2 reveal differences in requirements for entry of various alphaherpesviruses and for necrin-necrin interactions.

Struyf Frank; Martinez Wanda M; Spear Patricia G; et al

Department of Microbiology-Immunology, The Feinberg School of Medicine,

Northwestern University, 320 E. Superior Street, Chicago, IL 60611, USA.
Journal of virology (United States) Dec 2002, 76 (24) p12940-50,
ISSN 0022-538X Journal Code: 0113724
Contract/Grant No.: F32 GM 19765; GM; NIGMS; R01 AI 49394; AI; NIAID; R37 AI 36293; AI; NIAID; +

Document type: Journal Article

Language: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Necrin-1 and necrin-2 are related molecules that can function with different specificities as entry receptors for mammalian alphaherpesviruses through interaction with viral glycoprotein D (gD). The normal function of members of the necrin family is to mediate cell-cell adhesion through homotypic and heterotypic necrin-necrin interactions in cadherin-based adherens junctions. We examined mutations in three equivalent regions of the N-terminal V-like domains of necrin-1 and necrin-2 to test the effects on entry of various alphaherpesviruses, necrin-necrin interactions, and interactions of the mutant necrins with gD. Mutations in region I previously shown to severely impair herpes simplex virus (HSV) entry activity, but not pseudorabies virus (PRV) or bovine herpesvirus 1 (BHV-1) entry, did not reduce homotypic trans interactions for either necrin-1 or necrin-2 or binding of necrin-3 to necrin-1. Mutations in region II, patterned after a reported single-nucleotide polymorphism in necrin-2, enhanced intracellular accumulation of both necrin-1 and necrin-2 and had a deleterious effect on all of the activities under study. Mutations in region III previously shown to reduce homotypic trans interactions of necrin-2 impaired the entry of PRV and BHV-1 when introduced into either necrin-1 or necrin-2, but only the necrin-2 mutation reduced HSV entry activity. Binding of necrin-1 to necrin-3 was not affected. Effects of the necrin-1 and necrin-2 mutations on interactions with gD did not necessarily correlate with entry activity of the mutant receptors. We can conclude that structural requirements for HSV entry, PRV and BHV-1 entry, and homotypic and heterotypic trans interactions are all different despite the previously reported ability of HSV and HSV gD to inhibit trans interactions.

Record Date Created: 20021119

Record Date Completed: 20021219

?log hold

14may03 11:45:53 User208669 Session D2288.2

\$12.26 3.832 DialUnits File155

\$0.00 154 Type(s) in Format 6

\$2.31 11 Type(s) in Format 7

\$2.31 165 Types

\$14.57 Estimated cost File155

\$6.30 TELNET

\$20.87 Estimated cost this search

\$21.15 Estimated total session cost 3.913 DialUnits

Logoff: level 02.14.01 D 11:45:54

? b 155,357

28aug02 09:50:03 User208669 Session D2092.2

\$0.12 0.037 DialUnits File155

\$0.12 Estimated cost File155

\$0.30 0.037 DialUnits File359

\$0.30 Estimated cost File359

OneSearch, 2 files, 0.074 DialUnits FileOS

\$0.01 TELNET

\$0.43 Estimated cost this search

\$0.78 Estimated total session cost 0.172 DialUnits

SYSTEM: OS - DIALOG OneSearch

File 155: MEDLINE(R) 1966-2002/Aug W4

*File 155: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 357: Derwent Biotech Res. 1982-2002/June W1

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*File 357: File enhancements now online. See HELP NEWS 357.

Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set Items Description

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? ds

Set Items Description

S1 206 COXSACKIE AND RECEPTOR

S2 220222 TERMINUS OR TERMINAL

S3 9 S1 AND S2

S4 156542 DOMAIN OR DOMAINS

S5 38 S1 AND S4

S6 29 RD (unique items)

? t s3/7/2

3/7/2 (Item 2 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

11290763 21326079 PMID: 11316797

Multiple regions within the coxsackievirus and adenovirus receptor cytoplasmic domain are required for basolateral sorting.

Cohen C J, Gaetz J, Ohman T, Bergelson J M

Division of Immunologic and Infectious Diseases, The Children's Hospital of Philadelphia, Philadelphia, PA 19104-4318, USA. cohenc@email.chop.edu

Journal of biological chemistry (United States) Jul 6 2001, 276 (27)

p25392-8, ISSN 0021-9258 Journal Code: 2985121R

Contract/Grant No.: HL54734; HL; NHLBI; T32 AI07278; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The coxsackievirus and adenovirus receptor (CAR) mediates attachment and

infection by coxsackie B viruses and many adenoviruses. In human airway epithelia, as well as in transfected Madin-Darby canine kidney cells, CAR is expressed exclusively on the basolateral surface. Variants of CAR that lack the cytoplasmic domain or are attached to the cell membrane by a glycosylphosphatidylinositol anchor are expressed on both the apical and basolateral surfaces. We have examined the localization of CAR variants with progressive truncations of the cytoplasmic domain, as well as with mutations that ablate a potential PDZ (PSD95/dlg/ZO-1) interaction motif and a putative tyrosine-based sorting signal. In addition, we have examined the targeting of two murine CAR isoforms, with different C-terminal sequences. The results suggest that multiple regions within the CAR cytoplasmic domain contain information that is necessary for basolateral targeting.

Record Date Created: 20010702

? t s6/7/7 15 17 22 27

6/7/7 (Item 7 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

12604321 21547769 PMID: 11688979

Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptor.

Thioelen I, Keyaerts E, Lindberg M, Van Ranst M

Laboratory of Clinical and Epidemiological Virology, University of Leuven, Belgium.

Biochemical and biophysical research communications (United States) Nov 9 2001, 288 (4) p805-8, ISSN 0006-291X Journal Code: 0372516

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Non-human adenoviruses such as bovine adenovirus type 3 (BAV-3) that do not replicate in human cells but can infect human cells in culture could provide an attractive alternative to human adenoviral vectors for gene therapy. In addition, a large-animal model for genetic diseases can be very useful for the assessment of the efficacy of adenovector-mediated gene delivery in man. Recombinant human subgroup C adenovectors use the coxsackie and adenovirus receptor (CAR) to enter their target cells.

Through RT-PCR and sequencing we determined the complete coding sequence of bovine CAR which serves as the primary adenoviral attachment site on bovine cells. A multiple sequence alignment, involving all the previously identified CAR species (man, mouse, rat, pig, and dog) showed that bovine CAR was most related to porcine CAR (92% nucleotide similarity) and demonstrated a highly conserved adenovirus binding Ig1 domain. Copyright 2001 Academic Press.

Record Date Created: 20011105

6/7/15 (Item 15 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

11071013 21093138 PMID: 11177539

Manipulation of the cytoplasmic and transmembrane domains alters cell surface levels of the coxsackie-adenovirus receptor and changes the efficiency of adenovirus infection.

van't Hof W, Crystal R G

Division of Pulmonary and Critical Care Medicine, Weill Medical College of Cornell University, New York, NY 10021, USA.

Human gene therapy (United States) Jan 1 2001, 12 (1) p25-34, ISSN 1043-0342 Journal Code: 9008950

Contract/Grant No.: HL51746-06A1; HL; NHLBI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Expression of the coxsackie-adenovirus receptor (CAR) is a critical determinant in cellular susceptibility to infection with adenovirus-based gene transfer vectors. This study is focused on the hypothesis that manipulation of the cytoplasmic tail and transmembrane regions of CAR can be used to change cell surface levels of CAR and, consequently, to alter the efficiency of Ad-mediated gene transfer. To accomplish this, Flag-tagged ([F]) human CAR ([F]CAR), [F]tailless-CAR (lacking the cytoplasmic tail), and [F]GPI-CAR (containing a GPI lipid anchor instead of the transmembrane and cytoplasmic regions) were exogenously expressed in CHO cells. Analysis of (125I)-labeled anti-Flag antibody binding to transfected cells revealed that [F]tailless-CAR and [F]GPI-CAR were expressed on the cell surface in 1.8- to 2.5-fold higher amounts than [F]CAR, while the total expression levels were similar. Infection with replication-deficient adenovirus encoding beta-galactosidase (Ad-betaGal) demonstrated 1.5- to 2-fold higher levels of transgene expression in CHO cells expressing [F]tailless-CAR or [F]GPI-CAR, respectively, compared with cells containing [F]CAR. The form of CAR expressed did not affect the transport of fluorescent Cy3-Ad particles from the cell surface to the nuclear region. These observations indicate that transduction of target cells by Ad vectors can be optimized by increasing cell surface levels of CAR through functional deletion of the tail and membrane protein domains.

Record Date Created: 20010222

6/7/17 (Item 17 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

10511152 20036898 PMID: 10567268

Structural analysis of the mechanism of adenovirus binding to its human cellular receptor, CAR.

Bewley M C, Springer K, Zhang Y B, Freimuth P, Flanagan J M

Biology Department, Brookhaven National Laboratory, Upton, NY 11973, USA. Science (UNITED STATES) Nov 19 1999, 286 (5444) p1579-83, ISSN 0036-8075 Journal Code: 0404511

Contract/Grant No.: 1P41 RR12408-01A1; RR; NCRR

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Binding of virus particles to specific host cell surface receptors is known to be an obligatory step in infection even though the molecular basis for these interactions is not well characterized. The crystal structure of the adenovirus fiber knob domain in complex with domain I of its human cellular receptor, coxsackie and adenovirus receptor (CAR), is presented here. Surface-exposed loops on knob contact one face of CAR, forming a high-affinity complex. Topology mismatches between interacting surfaces create interfacial solvent-filled cavities and channels that may be targets for antiviral drug therapy. The structure identifies key determinants of binding specificity, which may suggest ways to modify the tropism of adenovirus-based gene therapy vectors.

Record Date Created: 19991209

6/7/22 (Item 22 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

10092971 99077161 PMID: 9862345

CTX, a *Xenopus* thymocyte receptor, defines a molecular family conserved throughout vertebrates.

Chretien J, Marcuz A, Courtet M, Kavevuo K, Vainio O, Heath J K, White S J, Du Pasquier L

Basel Institute for Immunology, Switzerland.

European journal of immunology (GERMANY) Dec 1998, 28 (12) p4094-104, ISSN 0014-2980 Journal Code: 1273201

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

CTX, a cortical thymocyte marker in *Xenopus*, is an immunoglobulin superfamily (IgSF) member comprising one variable and one constant C2-type IgSF domain, a transmembrane segment and a cytoplasmic tail. Although resembling that of the TCR and immunoglobulins, the variable domain is not encoded by somatic rearrangement of the gene but by splicing of two half-domain exons. The C2 domain, also encoded by two exons, has an extra pair of cysteines. The transmembrane segment is free of charged residues, and the cytoplasmic tail (70 amino acids) contains one tyrosine and many glutamic acid residues. ChT1, a chicken homologue of CTX, has the same structural and genetic features, and both molecules are expressed on the thymocyte surface. We cloned new mouse (CTM) and human (CTH) cDNA and genes which are highly homologous to CTX/ChT1 but not lymphocyte specific. Similarity with recently described human cell surface molecules, A33 antigen and CAR (coxsackie and adenovirus 5 receptor), and a number of expressed sequence tags leads us to propose that CTX defines a novel subset of the IgSF, conserved throughout vertebrates and extending beyond the

immune system. Strong homologies within vertebrate sequences suggest that the V and C2 CTX domains are scions of a very ancient lineage.

Record Date Created: 19990105

6/7/27 (Item 5 from file: 357)

DIALOG(R)File 357:Derwent Biotech Res.

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0256200 DBA Accession No.: 2000-10690

Ectodomain of coxsackie virus and adeno virus receptor genetically fused to epidermal growth factor mediates adeno virus targeting to epidermal growth factor receptor-positive cells - human adeno virus vector cell targeting improvement by epidermal growth factor and coxsackie virus and adeno virus receptor fusion protein for improved gene therapy

AUTHOR: Dmitriev I; Kashentseva E; Rogers B E; Krasnykh V; +Curriel D T
CORPORATE AFFILIATE: Univ.Alabama

CORPORATE SOURCE: Division of Human Gene Therapy, Dept. of Medicine, Pathology and Surgery, Gene Therapy Center, University of Alabama at Birmingham, 1824 6th Ave., South Room WTI 620, Birmingham, AL 35294-3300, USA. email:david.curriel@ccc.uab.edu

JOURNAL: J.Virol. (74, 15, 6875-84) 2000

ISSN: 0022-538X CODEN: JOVIAM

LANGUAGE: English

ABSTRACT: Use of adeno virus (AV) vectors for gene therapy is limited by low efficiency of AV-mediated gene transfer to target cells expressing marginal levels of AV fiber receptor. AV vectors could be improved by modifying AV tropism to target the virus to specific organs/tissues. The fact that the coxsackie virus and AV receptor (CAR) does not play a role in virus internalization, but acts as the virus attachment site, suggests that the extracellular part of CAR may be used to block the receptor recognition site of the AV fiber knob domain. Bispecific fusion proteins may be designed by a recombinant soluble form of truncated CAR (sCAR) and a targeting ligand. sCAR was genetically fused with human epidermal growth factor (EGF) and studied with respect to its ability to target AV infection to the EGF receptor overexpressed on cancer cell lines. sCAR-EGF protein bound to AV virions and directed them to EGF receptor, thereby achieving targeted delivery of reporter gene. sCAE-EGF protein is able to retarget AV via a non-CAR pathway, with attachment of gene transfer efficiency. (55 ref)

? log hold

28aug02 09:58:35 User208669 Session D2092.3

\$2.82 0.881 DialUnits File155

\$0.00 28 Type(s) in Format 6

\$1.05 5 Type(s) in Format 7

\$1.05 33 Types

\$3.87 Estimated cost File155

\$4.03 0.236 DialUnits File357

\$0.00 10 Type(s) in Format 6

\$2.70 1 Type(s) in Format 7

\$2.70 11 Types

\$6.73 Estimated cost File357

OneSearch, 2 files, 1.117 DialUnits FileOS

\$1.95 TELNET

\$12.55 Estimated cost this search

\$13.33 Estimated total session cost 1.289 DialUnits

Logoff: level 02.08.23 D 09:58:35

Reconnected in file OS 28aug02 10:28:19

SYSTEM:OS - DIALOG OneSearch

File 155:MEDLINE(R) 1966-2002/Aug W4

*File 155: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 357:Derwent Biotech Res. 1982-2002/June W1

(c) 2002 Thomson Derwent & ISI

*File 357: File enhancements now online. See HELP NEWS 357.

Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set Items Description

? ds

Set Items Description

S1 206 COXSACKIE AND RECEPTOR

S2 220222 TERMINUS OR TERMINAL

S3 9 S1 AND S2

S4 156542 DOMAIN OR DOMAINS

S5 38 S1 AND S4

S6 29 RD (unique items)

S7 159047 CYTOPLASM?

S8 14 S1 AND S7

? log hold

28aug02 10:30:02 User208669 Session D2092.4

\$0.90 0.282 DialUnits File155

\$0.00 10 Type(s) in Format 6

\$0.00 10 Types

\$0.90 Estimated cost File155

\$1.36 0.080 DialUnits File357

\$0.00 4 Type(s) in Format 6

\$0.00 4 Types

\$1.36 Estimated cost File357

OneSearch, 2 files, 0.361 DialUnits FileOS

\$0.43 TELNET

\$2.69 Estimated cost this search

\$2.69 Estimated total session cost 0.361 DialUnits

Logoff: level 02.08.23 D 10:30:02

? b 155,357

28aug02 11:02:35 User208669 Session D2093.1

\$0.28 0.081 DialUnits File1

\$0.28 Estimated cost File1

\$0.01 TELNET

\$0.29 Estimated cost this search

\$0.29 Estimated total session cost 0.081 DialUnits

SYSTEM:OS - DIALOG OneSearch

File 155: MEDLINE(R) 1966-2002/Aug W4

*File 155: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 357: Derwent Biotech Res. 1982-2002/June W1

(c) 2002 Thomson Derwent & ISI

*File 357: File enhancements now online. See HELP NEWS 357.

Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set Items Description

? s acvrp

S1 1 ACVRP

? t s1/7/1

1/7/1 (Item 1 from file: 357)

DIALOG(R) File 357: Derwent Biotech Res.

(c) 2002 Thomson Derwent & ISI. All rts. reserv.

0242449 DBA Accession No.: 1999-13214 PATENT

Isolated and purified polynucleotide useful for treating or preventing cancer, inflammation and virus disorders - recombinant virus-receptor protein production via vector-mediated gene transfer and expression in host cell for diagnosis, prevention, therapy and gene therapy

AUTHOR: Lal P, Corley N C

CORPORATE SOURCE: Palo Alto, CA, USA.

PATENT ASSIGNEE: Incyte-Pharm. 1999

PATENT NUMBER: US 5942606 PATENT DATE: 19990824 WPI ACCESSION NO.:

1999-493538 (1941)

PRIORITY APPLIC. NO.: US 979424 APPLIC. DATE: 19971124

NATIONAL APPLIC. NO.: US 979424 APPLIC. DATE: 19971124

LANGUAGE: English

ABSTRACT: An isolated and purified polynucleotide (I) which encodes a protein with the virus-receptor protein (ACVRP) sequence of 390 amino acids (specified), is new. Also claimed are: a composition containing (I); an isolated and purified polynucleotide fully complementary to (I); an isolated and purified polynucleotide (III); an isolated and purified polynucleotide fully complementary to (III); an expression

vector containing (I); a host cell transformed with the expression vector; and a method for detecting (I) in a biological sample containing nucleic acids, which consists of hybridizing the polynucleotide to the nucleic acids of the biological sample to form a hybridization complex and detecting the presence of the hybridization complex, therefore indicating the presence of the polynucleotide which encodes the protein in the sample. The administration of a vector which expressed a polynucleotide which is fully complementary to (I) may be useful for the prevention or treatment of cancer, a virus disorder or inflammation. The polynucleotides which encode ACVRP may be useful for diagnostic purposes and the expression vectors which encode ACVRP may be used for gene delivery. (28pp)

? b 155, 5

28aug02 11:03:18 User208669 Session D2093.2

\$0.21 0.066 DialUnits File155

\$0.21 Estimated cost File155

\$3.97 0.233 DialUnits File357

\$0.00 1 Type(s) in Format 6

\$2.70 1 Type(s) in Format 7

\$2.70 2 Types

\$6.67 Estimated cost File357

OneSearch, 2 files, 0.299 DialUnits FileOS

\$0.21 TELNET

\$7.09 Estimated cost this search

\$7.38 Estimated total session cost 0.380 DialUnits

SYSTEM:OS - DIALOG OneSearch

File 155: MEDLINE(R) 1966-2002/Aug W4

*File 155: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 5: Biosis Previews(R) 1969-2002/Aug W4

(c) 2002 BIOSIS

*File 5: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

Set Items Description

? ds

Set Items Description

S1 412 AU=LAL P?

S2 236 AU=CORLEY N?

S3 113 S1 AND S2

S4 940879 RECEPTOR

S5 4 S3 AND S4

S6 10480 CAR OR (COXSACKIE AND RECEPTOR?)

S7 110 HCAR OR MCAR

S8 10542 S6 OR S7

S9 397164 HOMOLOG?

S10 186 S9 AND S8

S11 134 RD (unique items)

S12 60 S4 AND S11

?1s5/7/3

5/7/3 (Item 3 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2002 BIOSIS. All rts. reserv.

12195930 BIOSIS NO.: 199900490779

Viral receptor protein.

AUTHOR: Lal Preeti(a); Corley Neil C

AUTHOR ADDRESS: (a)VISX Inc., Santa Clara, CA**USA

JOURNAL: Official Gazette of the United States Patent and Trademark Office

Patents 1225 (4):pNO PAGINATION Aug. 24, 1999

ISSN: 0098-1133

DOCUMENT TYPE: Patent

RECORD TYPE: Citation

LANGUAGE: English

? log hold

28aug02 11:07:46 User208669 Session D2093.3

\$3.78 1.180 DialUnits File155

\$0.00 61 Type(s) in Format 6

\$0.00 61 Types

\$3.78 Estimated cost File155

\$4.88 0.871 DialUnits Files

\$0.00 13 Type(s) in Format 6

\$1.75 1 Type(s) in Format 7

\$1.75 14 Types

\$6.63 Estimated cost Files

OneSearch, 2 files, 2.051 DialUnits FileOS

\$1.08 TELNET

\$11.49 Estimated cost this search

\$18.87 Estimated total session cost 2.431 DialUnits

Logoff: level 02.08.23 D 11:07:46

OM protein - protein search, using sw model

Run on: August 19, 2002, 16:13:17 ; Search time 57.91 Seconds
(without alignments)

updates/sec 748.036 Million cell

Title: US-09-902-759-39

Perfect score: 2012
Sequence: 1 MSLPGLVTNLLRFLGL.....SRMGAVPMVPAQSQAGSLV 390

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.032802.*
1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
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16: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*
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18: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
19: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2012	100.0	390	20	AAV27096	Human viral recept
2	2012	100.0	390	20	AAV13351	Amino acid sequenc
3	2012	100.0	390	20	AAV05286	EGF-like homologue
4	2012	100.0	390	21	AAV88574	Human PRO246 amino
5	2012	100.0	390	21	AAV94999	Human secreted pro
6	2012	100.0	390	22	AAV12340	Human PRO246 polyP
7	2012	100.0	390	22	AAV88358	Human membrane or
8	2012	100.0	390	22	AAV68599	PRO246. Homo sapi
9	2012	100.0	390	22	AAV31207	Amino acid sequenc
10	2012	100.0	390	22	AAV80219	Human PRO246 prote
11	2012	100.0	390	22	AAV53082	Human angiogenesis
12	2004	99.6	390	22	AAE06610	Human protein havi
13	2004	99.6	390	22	AAV90818	Human shear stress
14	2003	99.6	389	21	AAV76303	Fragment of human
15	1738.5	86.4	370	22	AAV65832	Human INTERCEPT
16	1736.5	86.3	370	22	AAV65906	Human secreted pro
17	1734.5	86.2	370	22	AAV65904	Human secreted pro
18	1734.5	86.2	370	22	AAV65905	Human secreted pro
19	1734.5	86.2	370	22	AAV65907	Human secreted pro
20	1601.5	79.6	341	22	AAV65833	Murine mature INTE
21	1581	78.6	321	22	AAV11937	Human viral recept
22	1581	78.6	321	22	AAV40551	Human polypeptide
23	1579	78.5	325	21	AAV59024	Human clone vcs1_1
24	1399	69.5	394	22	AAV65910	Murine secreted pr
25	1397	69.4	394	22	AAV65840	Murine secreted pr
26	1397	69.4	394	22	AAV65908	Murine secreted pr
27	1394	69.3	394	22	AAV65911	Murine secreted pr
28	1393	69.2	394	22	AAV65909	Murine secreted pr
29	1331	66.2	365	22	AAV65841	Murine mature INTE
30	1232	61.2	246	22	AAV65835	Murine INTERCEPT
31	1207	60.0	237	21	AAV76152	Human secreted pro
32	1107	55.0	220	22	AAV65872	Human INTERCEPT
33	1095	54.4	217	22	AAV65871	Human INTERCEPT
34	1027	51.0	206	22	AAV65870	Human INTERCEPT
35	965.5	48.0	212	20	AAV25748	Human secreted pro
36	890	44.2	177	22	AAV65867	Human INTERCEPT
37	833.5	41.4	249	22	AAV65843	Murine INTERCEPT
38	833	41.4	172	22	AAV38765	Human polypeptide
39	577	28.7	182	22	AAE05354	Mouse 10.3 kDa pro
40	467.5	23.2	120	22	AAV65846	Murine INTERCEPT
41	436	21.7	127	21	AAV95025	Human clone vcs1_1
42	400.5	19.9	99	22	AAV65837	Murine INTERCEPT
43	400	19.9	80	22	AAV65838	Murine INTERCEPT
44	367.5	18.3	426	22	AAV10359	Human CDNA SEQ ID
45	361.5	18.0	376	19	AAV57213	Mouse coxsackievir

ALIGNMENTS

RESULT 1
AAV27096
ID AAV27096 standard; Protein; 390 AA.

XX AC AAY27096;
XX DT 18-OCT-1999 (first entry)
XX DE Human viral receptor protein (ACVRP).
XX KW Viral receptor protein; ACVRP; cancer; viral disorder; inflammation;
XX KM gene therapy; human.
XX OS Homo sapiens.
XX PN US5942606-A.
XX PD 24-AUG-1999.
XX PF 24-NOV-1997; 97US-0979424.
XX PR 24-NOV-1997; 97US-0979424.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Corley NC, Lal P;
XX DR WPI; 1999-493538/41.
XX PS N-PSDB; AAX87000.
XX PT Isolated and purified polynucleotide useful for treating or
XX PT preventing cancer, inflammation and viral disorders
XX PS Claim 1; Fig 1A-D; 28pp; English.
XX CC This represents a human viral receptor protein (ACVRP). The protein
CC can be expressed by standard recombinant methodology. ACVRP can be used
CC for treating and/or preventing cancer, a viral disorder or inflammation
CC through the administration of a vector expressing a polynucleotide which
CC is fully complementary to the present sequence. Polynucleotides encoding
CC ACVRP can be used for diagnostic purposes to quantitate ACVRP expression
CC in biopsied tissues and correlate expression with disease. They can be
CC used to distinguish between the absence, presence and excess expression
CC of ACVRP and to monitor levels during therapeutic intervention.
CC Hybridisation probes can be used for mapping the naturally occurring
CC genomic sequence and detect differences in the chromosomal location in
CC normal, carrier or affected individuals. ACVRP may be ligated to a
CC heterologous sequence to produce a fusion protein which can be used to
CC screen peptide libraries for inhibitors of ACVRP activity and to screen
CC for novel antiproteoal and antifungal therapeutics. The expression
CC vectors which encode ACVRP can be used to deliver nucleotide sequences
CC to targeted organ, tissue or cell populations and complementary
CC polynucleotides to treat conditions associated with overexpression of
CC ACVRP by blocking transcription of the mRNA, modulating ACVRP activity
CC or regulating the gene function.

XX SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 20; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;

Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQQLHLHPANRLQAVEGSEVVLPAWYTLHGEV 60
Db 1 mislpgplvtcnllrflflglsalappsraqqlhlhpanrlqavegsevvlpawylhgev 60
QY 61 SSSQPEWEPFVWMFFKQKEKEDQVLSYINGVTTSKPQSVLSYVSMPSRNLSLRLEGIQEKD 120
Db 61 sssqpewepfvwmffkqkekedqvlsyinyngvttskpqsylvsmprnlslrlleglqekd 120
QY 121 SGPYSCSVNVQDKQKSRGHSIKTLELNLVLPAPPSCRLOQVPHYGANVTLSQSPRSK 180
Db 121 sgpyscsvnvqdkqkserghsiktlelnlvppappscrlogvphvganvtlscqsprsk 180
QY 181 PAVQYQWDRQLPSFQTFEPALDVIKRGSLSTNLSSMAGVYVCKAHNEVGTAQCNVTLE 240
Db 181 pavqyqwdrlpsfqtfepaldvirkrgslstnlssmagvyvckahnevgtaqcnvtle 240
QY 241 VSTGPGAAVAVGAVVGTLVGLIAGLVLYHRRGKALEBPANDIKEDAIAPRTLPMWPKS 300
Db 241 vstgpgaaavavavgtlvgliglvlyhrrgkaleebpandikedaiaprtlpmwps 300
QY 301 SDTISKNGTILSSVTSARALRPPHPRPGALTPTPELSSQALPSPRLPTTGCAHPQDIPSP 360
Db 301 sdtiskngtissvtsaralrpphprpgaltptpelssqalpsprlpttgahpqdipsp 360
QY 361 IPGVSSSGLSRMGAVPMVPAQSQAGSLV 390
Db 361 ipgvasssglsrmgavpmvpaqsgagslv 390

RESULT 2

AAY13351

ID AAY13351 standard; Protein; 390 AA.

XX AC AAY13351;

XX DT 25-JUN-1999 (first entry)

XX DE Amino acid sequence of protein PRO246.

XX KW Secreted protein; transmembrane protein; human; enterocolitis;

XX KW Zollinger-Ellison syndrome; gastrointestinal ulceration;

XX KW congenital microvillus atrophy; skin disease; cell growth;

XX KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;

XX KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;

XX KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;

XX KW anti-thrombotic; wound healing; tissue repair.

XX OS Homo sapiens.

XX PN WO9914328-A2.

XX PD 25-MAR-1999.

XX PF 16-SEP-1998; 98WO-US19330.

PR 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059113.
PR 17-SEP-1997; 97US-0059115.
PR 17-SEP-1997; 97US-0059117.
PR 17-SEP-1997; 97US-0059119.
PR 17-SEP-1997; 97US-0059121.
PR 17-SEP-1997; 97US-0059122.
PR 17-SEP-1997; 97US-0059184.
PR 18-SEP-1997; 97US-0059263.
PR 18-SEP-1997; 97US-0059266.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062287.
PR 21-OCT-1997; 97US-0063486.
PR 24-OCT-1997; 97US-0062814.
PR 24-OCT-1997; 97US-0062816.
PR 24-OCT-1997; 97US-0063045.
PR 24-OCT-1997; 97US-0063120.
PR 24-OCT-1997; 97US-0063121.
PR 24-OCT-1997; 97US-0063127.
PR 24-OCT-1997; 97US-0063128.
PR 27-OCT-1997; 97US-0063329.
PR 27-OCT-1997; 97US-0063327.
PR 28-OCT-1997; 97US-0063541.
PR 28-OCT-1997; 97US-0063542.
PR 28-OCT-1997; 97US-0063544.
PR 28-OCT-1997; 97US-0063549.
PR 28-OCT-1997; 97US-0063550.
PR 28-OCT-1997; 97US-0063564.
PR 29-OCT-1997; 97US-0063435.
PR 29-OCT-1997; 97US-0063704.
PR 29-OCT-1997; 97US-0063732.
PR 29-OCT-1997; 97US-0063738.
PR 29-OCT-1997; 97US-0063734.
PR 29-OCT-1997; 97US-0064215.
PR 29-OCT-1997; 97US-0063735.
PR 31-OCT-1997; 97US-0063870.
PR 31-OCT-1997; 97US-0064103.
PR 03-NOV-1997; 97US-0064248.
PR 07-NOV-1997; 97US-0064809.
PR 12-NOV-1997; 97US-0065186.
PR 17-NOV-1997; 97US-0065846.
PR 18-NOV-1997; 97US-0065693.
PR 21-NOV-1997; 97US-0066120.
PR 21-NOV-1997; 97US-0066364.
PR 24-NOV-1997; 97US-0066772.
PR 24-NOV-1997; 97US-0066466.
PR 24-NOV-1997; 97US-0066770.
PR 24-NOV-1997; 97US-0066511.
PR 24-NOV-1997; 97US-0066453.
XX
PA (GETH) GENENTECH INC.
XX
PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
XX
DR WPI; 1999-229533/19.
DR N-PSDB; AAX52221.
XX

PT New isolated human genes and polypeptides used in, e.g. treatment of
PT gastrointestinal ulceration
XX
PS Claim 12; Fig 17; 320pp; English.
XX
CC AA1Y3344-403 represent secreted and transmembrane human proteins.
CC The cDNA sequences are obtained from cDNA libraries, prepared from
CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
CC The encoded polypeptides have specific uses based on their homology to
CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
CC associated with the preservation and maintenance of gastrointestinal
CC mucosa and the repair of acute and chronic mucosal lesions
CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
CC ulceration and congenital microvillus atrophy), skin diseases associated
CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),
CC potent effects on cell growth and development, diseases related to
CC growth or survival of nerve cells including Parkinson's disease,
CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as
CC for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used
CC as a target for anti-tumor drugs. PRO533 may be used in the treatment
CC of Usher Syndrome or Atrophia areata; PRO269 can be used as an
CC anti-thrombotic agent; PRO287 polypeptides and portions may have
CC therapeutic applications in wound healing and tissue repair; PRO317 can
CC be used for treating problems of the kidney, uterus, endometrium, blood
CC vessels, or related tissue, e.g. in the heart of genital tract.
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 20; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MISLGPDLVNLRLFLGLSALAPSPRAQLQHLPANRLQAVEGSEVLPAWYTLHGEV 60
|||||
Db 1 mslpgrplvtlnlrlflglslalapsraqqlhpanrlqavegsevlpawtylthgev 60
QY 61 SSSQPEVFPFVWMPFKQKEKEQVLXYINGVTTSKPGVSLVYSMPSRNLSRLGLEQEKD 120
|||||
Db 61 sssqpwevpfvmwffkqkckedqvlvyingvttskpgvslvympsrnlsrlleglqekd 120
QY 121 SGPYSCSVNVDDKQKSRGHSKITLEANVLVPPAPSPCRLOGVPHVANVTISQSPRSK 180
|||||
Db 121 sgpyscsvnvddkqksrghsktlelanvlpapspcrlgcvphvanvtiscqspbrsk 180
QY 181 PAVOYOMDRQLPSFQTFAPAPALDIVRGLSLTNLSSMAGVYVCKAHNEVGTAQCNTLE 240
|||||
Db 181 pavqyqwdrlpsfqtffapaldvigrslsltnlssmagvyvckahnevgtaqcncvtle 240
QY 241 VSTGPAAVVAGAVGTLVGLIAGLVILVHRGKALAEPPANDIKEDAIAPRTLWPXKS 300
|||||
Db 241 vstgpaavvagavvgtlvlgilaglvllyhrrgkaleepandikedaiaprtlwpkps 300
QY 301 SDTISKNGTSSVTSAARALRPDPHPPRGALTPTPSLSSQALPSPRLPTTGAGHPDISP 360
|||||
Db 301 sdtiskngtssvtsaaralrpphprpgrgaltptpslssqalpsprlpttgahpdpisp 360

1 QY 361 IPGVSSSSGLSRMGAVPMVPAQSQAGSLV 390
|||||
Db 361 ipgvssssglsrmgavpmvpapqagagslv 390

RESULT 3

AAV05286

ID AAV05286 standard; Protein; 390 AA.

XX AAV05286;

XX 22-JUN-1999 (first entry)

DE EGF-like homologue PRO246.

XX Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261;
PRO246;

KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;
KW FGF-8 homologue.

XX Homo sapiens.

XX WO914327-A2.

XX 25-MAR-1999.

PF 10-SEP-1998; 98WO-US18824.

PR 25-NOV-1997; 97US-0066840.

PR 17-SEP-1997; 97US-0059114.

PR 17-SEP-1997; 97US-0059117.

PR 18-SEP-1997; 97US-0059263.

PR 15-OCT-1997; 97US-0062125.

PR 17-OCT-1997; 97US-0062285.

PR 17-OCT-1997; 97US-0062287.

PR 24-OCT-1997; 97US-0062816.

PR 29-OCT-1997; 97US-0063704.

PA (GETH) GENENTECH INC.

PI Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA;
PI Roy M, Wood WI;

DR WPI; 1999-229532/19.

DR N-PSDB; AAX28436.

XX Antibodies against specific proteins overexpressed in tumours

PS Example 1; Fig 27; 130pp; English.

XX This sequence represents the EGF-like homologue PRO246.
CC The invention relates to antibodies (Ab) that bind to any of the
CC polypeptides (I) designated PRO187; PRO533; PRO214; PRO240; PRO211;
CC PRO230; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit
CC expression and/or activity of (I) are used: (i) to inhibit growth of
CC tumours; and (ii) as diagnostic/prognostic reagents for detection or
CC quantification of (I) in cells or tissues, by standard immunoassays,
with

CC overexpression being indicative of cancer. For therapeutic use, the Ab
CC may be conjugated to a toxin, chemotherapeutic agent or radioisotope.
CC Genes expressing (I), many of which are growth factor homologues, are
CC overexpressed in some cases of cancer.

XX Sequence 390 AA:

Query Match 100.0%; Score 2012; DB 20; Length 390;

Best Local Similarity 100.0%; Pred. No. 5,8e-143;

Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps

0;

QY 1 MTSLPGLVTNLLRFLFLGLSALAPPSRAQLQLHPANRLQAVEGSEVLPAPWYTLHGEV 60
|||||

Db 1 mislpplvtlnllrflflglalsapstragqlhlpnrlqavegsevlpawyltlhgev 60

QY 61 SSSQPEVPFVNMWFQKEKEQDOVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGQEKD 120
|||||

Db 61 ssqpevpfvmwffkqkekedqvlsvyngvtctskpgvslvympsrnlslrlglqekd 120

QY 121 SGPPSCSVNVODKQKGRGHSIKTLEINLVLPAPPSGRLQGVPHGANVTLSQSPRSK 180
|||||

Db 121 sgppscsvnvodkqgkgrghsiktelnlvppapscrlgvyphganvltscqsprsk 180

QY 181 PAVQYQMDRQLPSFQTFPAPALDVIRGSLSTNLSSMAGVYVCKAHNEVGTAQCNTLE 240
|||||

Db 181 pavqyqwdrlpsfqtffapaldivrgslstnlssmagvyvckahnevgtacnvtle 240

QY 241 VSTGPGAAVVAGVGTVLVGLLGLVLVYHRGKALEEPANDIKEDAIAPRTLPMWPKS 300
|||||

Db 241 vstgpgaavvagavgtvlvlgllglvllyhrrgkaleepandikedaiaprtlpwps 300

QY 301 SDTISKNGTLLSVTSARALRPHGPPRRGALPTPTSLSSQALPSRLPTTDGHPQPRISP 360
|||||

Db 301 sdtsknngtlssvtsaralrphgpprrgalptptslssqalpsrllpttdgahpqprisp 360

QY 361 IPGVSSSSGLSRMGAVPMVPAQSQAGSLV 390
|||||

Db 361 ipgvssssglsrmgavpmvpapqagagslv 390

RESULT 4

AAV88574

ID AAV88574 standard; Protein; 390 AA.

XX AAV88574;

DT 09-AUG-2000 (first entry)

DE Human PRO246 amino acid sequence.

XX Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261;
PRO246;

KW PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human;
cell growth; proliferation; cell surface virus receptor; ADEPT;
KW antibody dependent enzyme mediated prodruq therapy.

```

7 OS Homo sapiens.
XX
XX WO200015666-A2.
XX
XX 23-MAR-2000.
XX
XX 08-SEP-1999; 99WO-US20594.
XX
XX 10-SEP-1998; 98US-0099803.
XX 10-SEP-1998; 98WO-US18824.
XX
XX (GETH ) GENENTECH INC.
XX
XX Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI, Botstein D;
XX
XX WPI; 2000-271386/23.
XX N-PSDB; AAA30052.
XX
XX New isolated antibodies which bind to specific polypeptides used for
PT diagnosis and treatment of neoplastic cell growth and proliferation -
XX
XX Example 8; Fig 16; 200pp; English.
XX
XX This sequence represents a human PRO246 amino acid sequence. PRO246 is
CC probably a cell surface virus receptor. The invention relates to
isolated
CC antibodies which bind to a polypeptide. The "PRO" polypeptides are
CC encoded by genes which are over expressed in the genome of tumour cells.
CC Vectors and host cells comprising the nucleic acid encoding the
CC antibodies are used in the production of the antibodies. The antibodies
CC and nucleic acids encoding them are used for diagnosing a tumour in a
CC mammal. The antibodies are used for inhibiting the growth of tumour
cells
CC and identifying compounds that inhibit a biological or immunological
CC activity of and/or expression of a PRO187, PRO533, PRO214, PRO240,
CC PRO211, PRO230, PRO261, PRO246 or PRO317 polypeptide. The antibody can
be
CC used in antibody dependent enzyme mediated prodrug therapy (ADEPT) by
CC conjugating the antibody to a prodrug-activating enzyme which converts
a
CC prodrug to an anti-cancer drug. The antibodies can be fluorescently
CC labelled and monitored by light microscopy, flow cytometry or
fluorimetry
CC for diagnosis and prognosis of tumours.
XX
XX Sequence 390 AA;
SQ
Query Match 100.0%; Score 2012; DB 21; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps
0;
QY 1 MISLPGPLVNTNLRFLFLGLSALAPPSRAQQLHLPAFNRLQAVEGGEVVLPAWYTLHGEV 60
Db 1 mislpgplvntnlrflflglasalppraqqlhlpanrlqaveggevvlpawytlhgev 60
QY 61 SSSQPMWEVPFVWMFFKQKEKEDQVLSYINGVTTSKPGVSLVYSPSRNLSRLLEGIOEKD 120

```

```

Db 61 sssqpmwepvfvmwffkqkekedqvlsyinygttskpgvslvympsrnlsrllegioekd 120
QY 121 SGPYSCSVNVODKQGKSRGHSIKTLELNVLVPPAPPSCRLOGVPHGANVTLSCQSPRSK 180
Db 121 sgpyscsvnvodkqgksrghsiktlemnvlvppapppscrlogvphganvtlscqsprsk 180
QY 181 PAVQYQWDRQLPSFQTFEPAPLADVIRGSLSTNLSSMAGVYVCKAHNEVGTAQCNVTLE 240
Db 181 pavqyqwdrqpsfqtfepapldvirgslstnlssmagvyvckahnevgtacnvtle 240
QY 241 VSTGPGAAVVAGAVVGTLVGLIAGLVLLVYHRKGALEBPANDIKEDAIAPRTLPMWPKS 300
Db 241 vstgpgaavvagavvgtlvlgliaglvllvyhrkgaleepandikedaiaprtlpmwps 300
QY 301 SDTISKNGTILSSVTSARALRPDPHGPFRPGALTPTPSLSSQALPSPRLPTTGAPHPISP 360
Db 301 sdtiskngtllssvtsaralrphgpprpgaltptpslsqalpsprlpttdgahpqpisp 360
QY 361 IPGVSSSGLSRMGAVPMVPAQSQAGSLV 390
Db 361 ipgvsssglsrmgavpvmvpaqsqagslv 390

RESULT 5
AAV94999
ID AAV94999 standard; Protein; 390 AA.
XX
AC AAV94999;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human secreted protein vcs1_1, SEQ ID NO:38.
XX
XX Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW neurodegenerative disease; asthma; contraceptive.
XX
OS Homo sapiens.
XX
XX WO200011015-A1.
XX
XX 02-MAR-2000.
XX
XX 24-AUG-1999; 99WO-US19351.
XX
XX 24-AUG-1998; 98US-0097638.
XX 24-AUG-1998; 98US-0097659.
XX 09-SEP-1998; 98US-0099618.
XX 28-SEP-1998; 98US-0102092.
XX 25-NOV-1998; 98US-0109978.
XX 23-DEC-1998; 98US-0113645.
XX 23-DEC-1998; 98US-0113646.
XX 23-AUG-1999; 99US-0379246.
PA (ALPH-) ALPHAGENE INC.
XX

```

1 PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-224657/19.
XX
PT New secreted or transmembrane proteins and polynucleotides encoding
PT them, useful for treating neurodegenerative disorders, autoimmune
PT diseases and cancer -
XX
PS Claim 47; Page 296-297; 357pp; English.
XX
CC The invention relates to 40 human secreted proteins (AAV94981-Y95020),
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted
CC proteins of the invention include those that are thought to be only
CC partially secreted, i.e., transmembrane proteins. The proteins of the
CC invention may exhibit one or more activities selected from the
following:
CC cytokine activity; cell proliferation; differentiation; immune
CC modulation; haematopoiesis regulation; tissue growth activity;
CC activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic
CC and thrombolytic activity; anti-inflammatory activity; and tumour
CC inhibition activity. The proteins may be administered to patients as
CC vaccines, and the nucleotides may be used as part of a gene therapy
CC regime. Diseases or conditions that may be treated using the proteins or
CC nucleotides of the invention include autoimmune diseases; genetic
CC disorders; haemophilia; cardiovascular diseases; cancer; bacterial,
CC fungal and viral infections, especially HIV; multiple sclerosis;
CC rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;
CC insulin dependent diabetes mellitus; and allergic reactions such as
CC asthma and anaemia. They may also be used for treating wounds, burns,
CC ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease and amyotrophic
CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may
CC additionally be useful as contraceptives. Nucleic acid sequences of the
CC invention may be used in chromosome mapping, and as a source of
CC diagnostic primers and probes. The present sequence represents one of
the
CC 40 proteins of the invention.
CC
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 21; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MISLPGPLVTNLRLFLGLSALAPPSRAQLQMLPANRLQAVEGGEVVLPAWYTLHGEV 60
Db 1 mislpgplvtnlrlflglalsappraqlqlhpanrlqaveggevvlpawylhgev 60
QY 61 SSSQDWEVFPVMMFQKEKEDQVLSYINGVTTSPGVSLVSMPSRNLRLLEGIQEKD 120
Db 61 sssqdwefvmmfkkqekedqvlsyngvttskpvslivsmprnlrlleglqekd 120
QY 121 SGFVSCSVNVQDKGKSRGHSIKTELNLVLPAPPSCRIGVPHGANVTLSCSPRSK 180
Db 121 sgfvsctsvnvqdkgksgrgshsiktelnlvlpappscrigvphganvtlscqgsprsk 180

QY 181 PAVQYQWDRQLPSFQTFPAPALDVIRGSLSTNLSSMAGVYVCKAHNEVGTAQCNVTLE 240
Db 181 pavqyqwdrqlpstfqtffapaldvirgslstnlssmagvyvckahnevgtacqcnvtle 240
QY 241 VSTGPGAAVAVGAVGTLVGLGLAGLVLYHRRGKALEEPANDIKEDALPRTLWPMS 300
Db 241 vstgpgaaavavagavgtlvglglaglvlyhrrgkaleepandikedalprtltwpms 300
QY 301 SDTISKNGTSSVTSARALRPHPRPFGALITPTPSLSSQALPSPRLPTDGAHPQPISP 360
Db 301 sdtiskngtlssvtसारलरप्हरप्फगलितप्टपस्लससालपस्प्रलप्टदगाहपूपीस् 360
QY 361 IPGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
Db 361 ipgvsssglsarmgavpvmvpaqsgagslv 390

RESULT 6
AAU12340
ID AAU12340 standard; Protein; 390 AA.
XX
AC AAU12340;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO246 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal
muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32678.
XX

PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.

AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor- α (TNF- α) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.

Matches	390;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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7

RESULT	7
AAB88358	
ID	AAB88358 standard; Protein; 390 AA

DT 23-MAY-2001 (first entry)

Human: secretory protein: membrane protein: vaccine: gene therapy

XX
KW
Pneumaloid arthritis; diabetes

OS Homo sapiens

PN EP1067182-A2

PD 10-JAN-2001

PF 07-JUL-2000; 2000EP-0114090

PR 08-JUL-1999; 99JP-0194179

PR 02-MAY-2000; 2000JP-0183766

PA (HELI-) HELIX RES INST

PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K

DR WPI; 2001-093989/11
DR N-PSDB; AAF93785.

1
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development -
XX
PS Claim 1; SEQ ID 84; 609pp + CD ROM; English.
XX
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by
CC AAB88317 - AAB88419. Included in the invention are primers
CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate
the
CC cDNA sequences of the invention. The invention also includes methods for
CC the production of antibodies directed against the proteins, and cDNA
CC sequences, which can be used in vaccines. The polynucleotide sequences
CC can be used in gene therapy. The polynucleotide sequences and the
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate secretory
CC protein/membrane protein expression. The nucleic acids and complementary
CC sequences may also be used as DNA probes in diagnostic assays
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC presence of similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC polypeptides and their role in metabolism. The polypeptides may be used
CC as antigens in the production of antibodies against them and in assays
to
CC identify modulators (agonists and antagonists) of expression and
CC activity. The antibodies and antagonists may also be used as therapeutic
CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.
XX
SQ Sequence 390 AA:
Query Match 100.0%; Score 2012; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps
0;
QY 1 MISLPGLVTNLTLPFLFLGSLALAPPSRAQLHLIPANRLQAVEGGEVLPAMYTLHGEV 60
Db 1 mislpglvtncnlrlftflglalsalappstraqlqlhlpantlqaveggevlpawytlnhgev 60
QY 61 SSSQDWEVPMVMWFPRKQKEKDQVLSYINGVTSKPGVSLVSMPSRNLSLRLEGIQEKD 120
Db 61 sssqgwevpmvmwfprkqekedqvlsyinyngvtskpgvslvsmpsrnlslrliegqekd 120
QY 121 SGFVSCSVNVODKQGRSGHSIKTELNVLPAPPSCRILQGVPHYGANVTLSGSPRSK 180
Db 121 sgpyscsvnvodkqgksrghsiktelnlvlpappscriqgyphvganvltscgqprsk 180
QY 181 PAVOYQMDROLPSFQTFAPALDVTIRGSLSTNLSSMAGVYVCCAHNVEGTAQCNTLE 240
Db 181 pavgyqwdrlpsfqtffapaldvirgslstnlssmagvyvckahnevgaqlacnvtle 240
QY 241 VSTGPAAVAVGAVVGTLVGLAGLAVLLVYHRKGALEBPANDIKEDAIAPRTLWP 300

Db 241 vstgpgaaavagavvgtlvglaglvllvyrkgaleebandikedaiaprtlpwps 300
QY 301 SDTISKNGTSSVTSARALRPHGPRPGALTPTPSISSQALPSPRLPTTDGAHPQIPSP 360
Db 301 sdtiskngtssvtsaralrphgprpgaltptpslssqalpsprlpttdgahpqipsp 360
QY 361 IPGVSSTGLSRMGAVPMVPAQSQAGSLV 390
Db 361 ipgvssstglstrmgavpmvpaqsgagslv 390
RESULT 8
AAB68599
ID AAB68599 standard; Protein; 390 AA.
XX
AC AAB68599;
XX
DT 27-APR-2001 (first entry)
XX
DE PRO246.
XX
KW Cytostatic; PRO protein; tumour; cancer.
XX
OS Homo sapiens.
XX
PN MO200105836-A1.
XX
PD 25-JAN-2001.
XX
PF 20-DEC-1999; 99WO-US30999.
XX
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28564.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI;
XX
XX WPI; 2001-091968/10.
DR N-PSDB; AAF60372.
DR
XX
PT New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,
PT useful for diagnosing and treating cancers -
XX
PS Claim 61; Fig 16; 196pp; English.
XX
CC The present invention relates to PRO proteins and coding sequences. The
CC present sequence is one such PRO protein. It was found that the PRO
genes
CC are amplified in the genome of tumour cells. The gene amplification is

PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
PR 07-DEC-1999; 99US-0169495.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2001-050091/06.
DR N-PSDB; AAC87040.
XX
PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
PT of related polypeptides -
XX
PS Claim 12; Fig 56; 244pp; English.
XX
CC The present sequence represents a human secreted and transmembrane
CC polypeptide. The specification describes human polypeptides, designated
CC PRO196, PRO444, PRO183, PRO210, PRO215, PRO217, PRO242, PRO288,
CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC can be modulated with agents that bind to these polypeptides, resulting
CC in the death of the cells. The polynucleotides encoding these
CC polypeptides are useful in the recombinant production of the
CC polypeptides, as a hybridisation probe to screen libraries to isolate
CC homologous sequences, or to map the gene. They may also be used for
CC analysing genetic disorders, and to produce transgenic animals which are
CC useful for the development and screening of therapeutically useful
CC reagents. The polynucleotides can also be used in gene therapy e.g. to
CC replace a defective gene.
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPGPLVTNLRLFLGLSALAPPSRAQLQLHLDPANRLQAVEGGEVILPAWYTLHGEV 60

Db 1 mslpgplvtnlrlflfiglsalapparaqqlhlpnrlqaveggevllpawytlhgev 60
QY 61 SSSQPEVFPVWMEFKQKEKEDQVLSTYINGVTTSPGVSLVYSMPSRNLSLRLGLEQEKD 120
Db 61 sssqpewpfvwmefkqkekedqvlstyngvttspgvslvyssmpsrnlsrlrlgleqekd 120
QY 121 SGPPSCSVNVODKQSGSRGHSIKTLEINLVPPAPPSCRLOGVPHVGANVTLSQSPRSK 180
Db 121 sgppscsvnvodkqsgsrghsiktlelnlvppappscrlogvphvganvtlscqsprsk 180
QY 181 PAVQYQMDRQLPSFQTEFAPALDIVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE 240
Db 181 pavqyqmdrqlpsfqtetfapaldivirgslsltnlssmagyvyvckahnevgtaqcnvtle 240
QY 241 VSTPGAAVAVAGAVGTGLVGLAGLVLVHRRGKALEEPANDIKEDAIAPRTLPMPKS 300
Db 241 vstpgaaavavagavgtglvgllagvlvlyhrrgkaleepandikedaiaprtlpmpk 300
QY 301 SPTISKNGTLLSVTSARALRPHPGPRRGALTPTPSSQALPSPRLPTDGAHPOPISP 360
Db 301 sptiskngtllsvtsaralrphpgprrgaltpptpsqalpsprlptdgaahpopisp 360
QY 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
Db 361 ipgvsassglstrmgavpvmvpagsgagslv 390

RESULT 10

AAB80219
ID AAB80219 standard; Protein; 390 AA.
XX
AC AAB80219;
XX
DT 24-APR-2001 (first entry)
XX
DE Human PRO246 protein.
XX
KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation.
XX
OS Homo sapiens.
XX
PN WO200104311-A1.
XX
PD 18-JAN-2001.
XX
PF 22-FEB-2000; 2000WO-US04414.
XX
PR 07-JUL-1999; 99US-0143048.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 05-JAN-2000; 99WO-US00219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Botstein D, Deenoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin LJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WT;
 XX
 DR WPI; 2001-081051/09.
 DR N-PSDB; AAF72379.
 XX
 PT Sixty one nucleic acids encoding PRO polypeptides which are useful in
 PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
 PT Alzheimer's disease) -
 XX
 PS Claim 1; Fig 17; 393pp; English.
 XX
 CC The present sequence is one of sixty one novel secreted and
 CC transmembrane PRO polypeptides. The PRO polypeptides are
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
 CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
 CC endometrial bleeding angiogenesis, ischaemia such as coronary
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
 CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
 CC diabetes and retinal disorders such as retinitis pigmentosum.
 CC The PRO nucleic acids have applications in molecular biology, including
 CC use as hybridization probes, and in chromosome and gene mapping.
 XX
 SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 22; Length 390;
 Best Local Similarity 100.0%; Pred. No. 5.8e-143;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps

0;
 QY 1 MISLPGPLVNTLRLFLGLSALAPPSRAQLHLPLNRQLQAVEGGEVLLPAMYTLTGEV 60
 Db 1 mislpgplvntlrlflglalsalapsraqqlhpanrlqaveggevllpawtclhgev 60
 QY 61 SSSQPEWVFPVMWFRKQKEKEDQVLSYINGVTTSKRGVSLVYSMPBRNLSRLBGLQEKD 120
 Db 61 sssqpewvfpvmwffkqkexedqvlsyngvttskrgvslvysmpbrnlsrlleglqekd 120
 QY 121 SGPYSGSVNVODKQKGRSHIKTLELNVLPAPPSCRLOGVPHVGANVTLSQGSPRSK 180

Db 121 sgpyscsvnmvdkgkgrshiktlelnvlpappscrlsgvphvganvltscqsprsk 180
 QY 181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTL 240
 Db 181 pavqyqwdrdqlpsfqtffapaldvirgslsltnlssmagvyvckahnevtaqcnvtle 240
 QY 241 VSTGPGAAVAVGAVGTLVGIGLAGIVLVLYHRRGKALEEPANDIKEDAIAPRTLPMWPKS 300
 Db 241 vstgpgaaavavavgtlvvgiglagivlvlyhrrgkaleepandikedaiaprtclpmwps 300
 QY 301 SDTISKNGTLLSVTSARALRPPHGPFRPGALTPTPSLSSQALPSPRUPTTGAHPORISP 360
 Db 301 sdtiskngtllsvtsaralrpphgpfrpgaltptpslssqalpsprlptdgahpdpisp 360
 QY 361 IPGGSVSSGLSRMGAVPVMVPAQSQAGSLV 390
 Db 361 ipgsvassglstrmgavpvmvpaqsgagslv 390

RESULT 11
 AAB53082
 ID AAB53082 standard; Protein; 390 AA.
 XX
 AC AAB53082;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human angiogenesis-associated protein PRO246, SEQ ID NO:96.
 XX
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 PN WO200053753-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 05-JAN-2000; 2000WO-US00219.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.

PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Masters SA;
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2001-090793/10.
DR N-PSDB; AAC97441.
XX
XX
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
PT genetic disorders and treating cardiovascular, endothelial or
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -
XX
XX
PS Claim 69; Fig 38; 293pp; English.
XX
CC The invention relates to novel human angiogenesis-associated proteins
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
CC PRO proteins. The invention also relates to vectors and host cells
CC comprising a PRO nucleic acid, the recombinant production of a PRO
CC protein, PRO antibodies specific for a PRO protein, fusion proteins
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
CC compounds which inhibit the expression of a PRO gene. The invention
CC additionally encompasses methods of identifying modulators of PRO
CC expression or activity; diagnosing a cardiovascular, endothelial or
CC angiogenic disorder, or a susceptibility to such a disorder by detecting
CC mutations in a PRO gene, or the expression level of a PRO gene within a
CC particular tissue; treating a cardiovascular, endothelial or angiogenic
CC disorder via the administration of a PRO protein, PRO nucleic acid, or
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising
a
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
CC administration of a PRO protein, or an agonist or antagonist thereof.
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
CC agonists and PRO antagonists may be used as therapeutic agents to treat
CC cardiovascular, endothelial or angiogenic disorders, such as
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
CC disease, or stroke. PRO nucleic acids are additionally useful in the
CC recombinant production of PRO proteins, as hybridisation probes to
CC screen libraries to isolate cDNAs with sequence identity to PRO
proteins,
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
CC gene therapy. PRO nucleic acids can also be used to produce transgenic
CC animals useful for the development and screening of potential
CC therapeutic agents. The present sequence represents a PRO protein of the
invention.
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 22; Length 390;

Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps
0;
QY 1 MISLPGLVTNLLRFLFLGLSALAPSPRAQLHLHPANRLQAVEGSEVLPAWYTLHGEV 60
|||||
Db 1 mislpplvtcnllrflflglalappsraqqlhlpnrlavegsevlpawtylhgev 60
QY 61 SSSQPEVFPFWMFFKQKEKEDQVLSTINGTTSKRGVSLVYSMPBRNLSRLGLEQEKD 120
|||||
Db 61 sssqpewepfvmwffkqkexedqvlsyngvltckpyslvysmpsrnlslrlglqekd 120
QY 121 SGPYSCSVNVODKQGRSGHSIKITELINVLVPPAPPCRLQGVPHVGANVTLSQSPRSK 180
|||||
Db 121 sgpyscsvnvdkqgrsgrhsikitlelnvlppappscrlgvpvhganvtlscgprsk 180
QY 181 PAVQYQWDRQLPSFQTFPAPALDIVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCWVTL 240
|||||
Db 181 pavqywdtrqlpsfqtffapaldvirgslsltnlssmagvyvckahnevgtacnvtle 240
QY 241 VSTGPAAVAVAGAVGTLVGLGLVLYHRRGKALEEPNANDIKEDAIAPRTLPWPKS 300
|||||
Db 241 vstgpaaavagavgtlvglglvlyhrrgkaleepndikedaiaprtlpwps 300
QY 301 SDTISKNGTSSVTSARALRPHGPPRGALTPTPSLSSQALPSPRUPTTGDGHPQRI 360
|||||
Db 301 sdtiskngtssvtsaaralrphgpprgaltptpslsgalpsprlptctgdahpqris 360
QY 361 IPGVSSSSGLSRMGAVPVMVPAQSQAGSLV 390
|||||
Db 361 ipgvsssglsrmgavpvmvpaqsgslv 390

RESULT 12
AAE06610
ID AAE06610 standard; Protein; 390 AA.
XX
AC AAE06610;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human protein having hydrophobic domain, HP10801.
XX
KW Human, hydrophobic domain; gene therapy; nutritional supplement;
cell proliferation; immunomodulatory; autoimmune disorder;
antimicrobial;
KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
KW contraceptive; antiinfectility; antiinflammatory.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT /label= Signal_peptide
FT Protein 31..390

FT /note= "Mature human protein with hydrophobic domain"
XX
PN WO200149728-A2.
PD 12-JUL-2001.
XX
PE 28-DEC-2000; 2000WO-JP09359.
XX
PR 06-JAN-2000; 2000JP-0000585.
PR 06-JAN-2000; 2000JP-0000588.
PR 11-JAN-2000; 2000JP-0002299.
PR 03-FEB-2000; 2000JP-0026862.
PR 03-MAR-2000; 2000JP-0058367.
XX
PA (PROT-) PROTEGENE INC.
PA (SAGA) SAGAMI CHEM RES CENT.
XX
PI Kato S, Kimura T;
XX
DR WPI; 2001-418355/44.
DR N-PsDB; AAD12605.
XX
PT Human proteins with hydrophobic domains and the nucleic acids encoding
PT them, useful for preventing diagnosing and treating e.g. cancer,
PT Alzheimer's and inflammation -
XX
PS Claim 1; Page 448-450; 563pp; English.
XX
CC The present sequence is human protein with hydrophobic domain,
CC HP10801. The polynucleotide and polypeptide of the invention
CC may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The
CC polynucleotides
CC may be used to produce the polypeptide, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the protein. The
CC polynucleotides and its complementary sequences may also be used as DNA
CC probes in diagnostic assays and also used in gene therapy. The
CC polypeptides may also be used as antigens in the production of
CC antibodies
CC and in assays to identify modulators of polypeptide expression and
CC activity. The polypeptides and nucleic acids may be used as nutritional
CC supplements, to modulate cytokine and cell proliferation activity, to
CC modulate immune stimulation or suppression (e.g. for the treatment of
CC microbial infections and autoimmune disorders such as multiple
CC sclerosis,
CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
CC haematopoiesis, to modulate tissue growth activity (e.g. for the
CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
CC disease), to modulate activin and inhibin activity (e.g. for controlling
CC fertility), to modulate chemotactic and chemokinetic activity, to
CC modulate haemostatic and thrombolytic activity, to modulate receptor
CC ligand activity, to modulate inflammation and to inhibit tumour growth.
XX
SQ Sequence 390 AA;

Query Match 99.6%; Score 2004; DB 22; Length 390;
Best Local Similarity 99.7%; Pred. No. 2.3e-142;

Matches 389; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MISLPGELVNTLIRFLFLGLSALAPSPRAQLOLHLPMANRLQAVEGSEVLPAMWYTLHGEV 60
DB 1 mislpgelvtlnllrflflglalappaadqlhlpanrlqavegsevlpaawtllhgev 60
OY 61 SSSQPEWEPFVMMFFKQKEKEDOVLSYINGVYTSKPGVSLVYSMPSENLSLRLEGIQEKD 120
DB 61 ssqpewepfvmmffkqkakedqvlsvyngvtskpgvslvyssmpsrnlslrllegiqekd 120
OY 121 SGPYSCSVNVQDKGKSRGHSIKTLELVLPAPAPSCRLQGVPHVGANVTLSQSPRSK 180
DB 121 sgpyscsvnvqdkgksrghsiktlevlpapapscrlqgvphganvtlscgsprrsk 180
OY 181 PAVQYQWDRQLPSFQTFPAPALDIVRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE 240
DB 181 pavqyqwdrqlpstfqtffapaldivrgslsltnlssmagvyvckahnevgtaqcnvtle 240
OY 241 VSTGPGAAVVAGAVVGTVLVGLGLAGLVLLVYHRGKALEEPANDIKEDAIAPRTLPMWPKS 300
DB 241 vstgpgaavvagavvgtvlvgllaglvllvhrgkaleepandikedaiaprtlpmwps 300
OY 301 SDTISKNGTSLSVTSARALRPHPGPRPGALTPTPSLSSQALPSRPLPTDGAHPQFISP 360
DB 301 sdtiskngtislsvtsaralrpphpgprpgaltptpslssqalpsrplptdga hpqfisp 360
OY 361 IPGVSSSSGLSRMGAVPVMVPAQSQAQSLV 390
DB 361 ipgvsssgslsrmgavpvmvpaqsqagslv 390

RESULT 13
AAB90818
ID AAB90818 standard; Protein; 390 AA.
XX
AC AAB90818;
XX
DT 15-JUN-2001 (first entry)
XX
DE Human shear stress-response protein SEQ ID NO: 144.
XX
KW Human; shear stress-response protein; vascular disease;
KW arteriosclerosis.
XX
OS Homo sapiens.
XX
PN WO200125427-A1.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-JP06840.
XX
PR 01-OCT-1999; 99JP-0280976.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (NOJIT/) NOJIMA H.
XX

PI Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
 PI Kuga T, Sekine S, Nakamura Y, Sugano S;
 XX
 DR WPI; 2001-266308/27.
 DR N-PSDB; AAH02949.
 XX
 PT DNA sequences, proteins encoded by them and antibodies against them
 PT useful in diagnosis and treatment of vascular disease caused by
 PT arteriosclerosis -
 XX
 PS Claim 35; Page 599-601; 678bp; Japanese.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human shear stress response proteins. These are useful in the
 CC diagnosis, treatment and screening of vascular diseases caused by
 CC arteriosclerosis, including heart failure, post-PTCA restenosis and
 CC hypertension.
 CC
 XX
 SQ Sequence 390 AA;
 0;
 Query Match 99.6%; Score 2004; DB 22; Length 390;
 Best Local Similarity 99.7%; Pred. No. 2.3e-142;
 Matches 389; Conservative 0; Mismatches 1; Indels 0; Gaps
 0;
 QY 1 MISLPGPLVTLRLRFLGLSALAPPSRAQIQHLHPANRLQAVEGGEVLLPAMYTLHGEV 60
 Db 1 mislpgplvtnllrlflglalsalappsraqqlhpanrlqavegeevllpawylthgev 60
 QY 61 SSSQMEVFPVWMFFKQKEKEDQVLSYINGVTTSKPQSVSLVSMPSRNLSLRLEQLQEKD 120
 Db 61 sssqmevfpvwmffkqkexkedqvlsyinyngvttskpsvslvsmprnlsrlrlgqlqekd 120
 QY 121 SGPYSCSVNVODKQGRSGHSIKTELINLVPPAPPSCRLOGVPHYGANVTLLSCQSPRSK 180
 Db 121 sgpyscsvnvodkqgrsghsiktelnlvppapppscrigvyphganvtlscqsprrsk 180
 QY 181 PAVQYQMDROLPSFQTFAPALDVIRGSLSTNLSSMAGVYVCKAHNEVGTAAQCNTLLE 240
 Db 181 pavqyqwdrlpsfqtffapaldvirtsisltnlssmagvyvckahnevgtlaqcntlle 240
 QY 241 VSTGPGAANVAVAGVVTLVGILGLVLLVYRRGKALEBPANDIKEDALAPRTLWPWPKS 300
 Db 241 vstgpgaavnavagvvtlvglglvllvyrrgkaleebpandikedalaptlwpwps 300
 QY 301 SDTISKNGTSSVTSARALRPHGPRRGALTPTPSLSSQALPSRPLPTTDGAHPQPISP 360
 Db 301 sdtiskngtssvtsaaralrphgpprgaltptpslssqalpsrplpttdgahpqpi 360
 QY 361 IPGVSSSGLSRMGAVVWVPAQSQAGSLV 390
 Db 361 ipgvsssglsrmgavvwvpaqsgagslv 390
 RESULT 14
 AAY76303
 ID AAY76303 standard; Protein; 389 AA.

XX AAY76303;
 AC 23-MAR-2000 (first entry)
 XX
 DT
 XX
 DE Fragment of human secreted protein encoded by gene 29.
 XX
 KW Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KW therapy.
 XX
 OS Homo sapiens.
 PN WO9958660-A1.
 XX
 PD 18-NOV-1999.
 XX
 PE 06-MAY-1999; 99WO-US09847.
 XX
 PR 12-MAY-1998; 98US-0085093.
 PR 12-MAY-1998; 98US-0085094.
 PR 12-MAY-1998; 98US-0085105.
 PR 12-MAY-1998; 98US-0085180.
 PR 18-MAY-1998; 98US-0085906.
 PR 18-MAY-1998; 98US-0085920.
 PR 18-MAY-1998; 98US-0085921.
 PR 18-MAY-1998; 98US-0085922.
 PR 18-MAY-1998; 98US-0085923.
 PR 18-MAY-1998; 98US-0085924.
 PR 18-MAY-1998; 98US-0085928.
 PR 18-MAY-1998; 98US-0085925.
 PR 18-MAY-1998; 98US-0085927.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
 PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR;
 PI Lafleur DW, Endress GA, Ebner R;
 XX
 DR WPI; 2000-062296/05.
 XX
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders -
 XX
 PS Disclosure; Page 440-441; 475pp; English.
 XX
 CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
 CC AAY76124 to AAY76223 are the secreted proteins encoded by the 97 human
 CC genes. This sequence represents a fragment of one of the human secreted
 CC proteins. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions,
 CC e.g. by protein or gene therapy. Also pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample

or by determining the presence of mutations in the new genes. Specific uses are described for each of the 97 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences shown in AAY76224 to AAY76424 represent fragments of the secreted proteins.

Sequence 389 AA;

Query Match 99.6%; Score 2003; DB 21; Length 389;
Best Local Similarity 99.7%; Pred. No. 2.7e-142;
Matches 388; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MISLPGELVTLRLFLGLSALAPPSRAQIOQLHPANRLQAVEGSEVVLPAWYTLHGEV 60
1 mislpgelvtlnrlflglisalappraqqlhpanrlqavegsevvlpawytlhgev 60
61 SSSQPMVEVPFVMMFFKQKEKEDQVLSYINGVTTSPGVSLVYSMPSRNLSLRLEGLQEKD 120
61 sssqpmvevpfvmwffkqkedqvlsyngvttspgvslyvsmpsrnlsrlrleqlqekd 120
121 SGPYSCSVNVODKQKSRGHSIKITLELNVLVPPAPPSCRLOGVPHVGANVTLSQSPRSK 180
121 sgpyscsvnvodkqksrgshsikitlelnvlvpappscrlgvyphganvtlscqpsrk 180
181 PAVQYOWDRQLPSFQTFPAPALDIVIRGSLSTNLSSMAGVYVCKAHNEVGTAQCNTVLE 240
181 pavqyowdrqlpsfqtfpapaldivirgslstnlssmagvyvckahnevgtacnvtle 240
241 VSTGPGAAVAVAGAVVGTLVGLLGLVLTLYRRGKALEEPANDIKEDAIAPRTLPPWPKS 300
241 vstgpgaaavavagavvgtlvglglvltlyrrgkaleepandikedaiaprtlppwps 300
301 SDTISKNGTSSVTSARALRRPHGPPRGALTPPSSLSQALPSRPLPTDGAHPQIPSP 360
301 sdtiskngtssvtsaeralrrphgpprgaltppsslsqalpsrplptdgaahpqipsp 360
361 IPGIVSSSGLSRMGAVPVMVPAQSQAGSL 389
361 ipgivsssglstrmgavpvmvpaqsgagsl 389

RESULT 15
AAB65832
ID AAB65832 standard; Protein; 370 AA.

AC AAB65832;

DT 28-MAR-2001 (first entry)

XX

DE Human INTERCEPT 258 SEQ ID NO: 28.

Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281; INTERCEPT 258; coronary disorder; olfactory disorder; neurological disorder; pulmonary disorder; immunological disorder; developmental disorder; kidney disorder.

Homo sapiens.

MO200078808-Al.

28-DEC-2000.

19-JUN-2000; 2000WO-US16883.

18-JUN-1999; 99US-0336536.

(MILL-) MILLENNIUM PHARM INC.

Leiby KR, McKay C, Bossone S;

WPI; 2001-050109/06.

New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple sclerosis and asthma -
Claim 9; Page 228-229; 332pp; English.

The present invention provides the protein and coding sequences of the human and murine secreted or transmembrane proteins TANGO 253, TANGO 257, TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.

Sequence 370 AA;

Query Match 86.4%; Score 1738.5; DB 22; Length 370;
Best Local Similarity 94.2%; Pred. No. 1.8e-122;
Matches 341; Conservative 3; Mismatches 11; Indels 7; Gaps 1;

1 MISLPGELVTLRLFLGLSALAPPSRAQIOQLHPANRLQAVEGSEVVLPAWYTLHGEV 60
1 mislpgelvtlnrlflglisalappraqqlhpanrlqavegsevvlpawytlhrev 60
61 SSSQPMVEVPFVMMFFKQKEKEDQVLSYINGVTTSPGVSLVYSMPSRNLSLRLEGLQEKD 120
61 sssqpmvevpfvmwffkqkedqvlsyngvttspgvslyvsmpsrnlsrlrleqlqekd 120
121 SGPYSCSVNVODKQKSRGHSIKITLELNVLVPPAPPSCRLOGVPHVGANVTLSQSPRSK 180
121 sgpyscsvnvodkqksrgshsikitlelnvlvpappscrlgvyphganvtlscqpsrk 180
181 PAVQYOWDRQLPSFQTFPAPALDIVIRGSLSTNLSSMAGVYVCKAHNEVGTAQCNTVLE 240


```
Db      181 pavqyqwdrqrpsfcffafapaldivrgslstnlssmagvyvckahnevgtacnvtlle   240
QY      241 VSTGPGAAVAVAGAVGTLLVGIGLGLVLLYHRRGKALEEPANDIKEDALPRTLWPKS    300
        |||               |||               |||               |||
Dd      241 vatgpgaaavaeavvgtlvglgllaglvlyhyrfgkaleepandikedalaprtlpwks    300
QY      301 SPTISKNGTLSSVT SARALRPDHGRPRRGALTPTPSLSQA LSPSR-----LPFTDGA    353
        |||             |||             |||             |||         | : | :
Dd      301 eatdkiskngtclsavtsaaralrprrhgprpprgaltptplsagalsprnhandrwpgrpstnip 360
QY      354 HP 355
        ||
Dd      361 hp 362
```

Search completed: August 19, 2002, 17:09:06
Job time: 3349 sec

OM protein - protein search, using sw model

Run on: August 19, 2002, 16:16:12 ; Search time 24.02 Seconds
(without alignments)

updates/sec 396.585 Million cell

Title: US-09-902-759-39

Perfect score: 2012

Sequence: 1 MISLPGLVTNLRFLFLGL.....SRMGAVPMVPAQSQAGSLV 390

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/2/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	2012	100.0	390	2	US-08-979-424-1		Sequence 1, Appli
2	353.5	17.6	365	4	US-08-928-383B-26		Sequence 26, Appli
3	346	17.2	365	4	US-08-928-383B-2		Sequence 2, Appli
4	345.5	17.2	365	4	US-08-928-383B-23		Sequence 23, Appli
5	343	17.0	365	2	US-08-979-424-3		Sequence 3, Appli
6	343	17.0	365	4	US-09-272-496-2		Sequence 2, Appli
7	297	14.8	319	1	US-08-597-495B-22		Sequence 22, Appli
8	297	14.8	319	4	US-09-068-051A-22		Sequence 22, Appli
9	290.5	14.4	365	4	US-08-928-383B-24		Sequence 24, Appli
10	289.5	14.4	387	4	US-09-175-928-2		Sequence 2, Appli
11	258	12.8	318	4	US-09-068-051A-32		Sequence 32, Appli

12	176	8.7	299	4	US-09-188-930-331	Sequence 331, App
13	176	8.7	299	4	US-09-462-270-2	Sequence 2, Appli
14	171	8.5	299	4	US-09-188-930-189	Sequence 189, App
15	158.5	7.9	501	2	US-08-408-095-31	Sequence 31, Appli
16	153.5	7.6	344	2	US-08-602-725-34	Sequence 3, Appli
17	152	7.6	1101	3	US-08-986-485-2	Sequence 12, Appli
18	134	6.7	607	2	US-08-752-307B-12	Sequence 12, Appli
19	133	6.6	321	6	5169835-17	Patent No. 5169835
20	133	6.6	464	2	US-08-602-725-32	Sequence 32, Appli
21	133	6.6	642	1	US-08-217-299-1	Sequence 1, Appli
22	133	6.6	698	2	US-08-602-725-36	Sequence 36, Appli
23	133	6.6	734	2	US-08-389-459A-17	Sequence 17, Appli
24	133	6.6	734	3	US-08-987-867A-17	Sequence 17, Appli
25	132.5	6.6	252	2	US-08-414-657D-56	Sequence 56, Appli
26	132.5	6.6	287	2	US-08-414-657D-48	Sequence 48, Appli
27	132.5	6.6	304	2	US-08-414-657D-44	Sequence 44, Appli
28	132.5	6.6	308	2	US-08-414-657D-46	Sequence 46, Appli
29	132.5	6.6	325	2	US-08-414-657D-2	Sequence 2, Appli
30	132.5	6.6	325	2	US-08-414-657D-41	Sequence 41, Appli
31	132.5	6.6	338	2	US-08-414-657D-60	Sequence 60, Appli
32	132.5	6.6	1241	4	US-09-040-774-2	Sequence 2, Appli
33	132	6.6	828	1	US-08-261-304-2	Sequence 2, Appli
34	130	6.5	1091	3	US-08-986-485-5	Sequence 5, Appli
35	129	6.4	917	1	US-08-245-295-2	Sequence 2, Appli
36	129	6.4	917	1	US-08-481-130-2	Sequence 2, Appli
37	129	6.4	917	1	US-08-656-984A-2	Sequence 2, Appli
38	129	6.4	917	1	US-08-485-604-2	Sequence 2, Appli
39	129	6.4	917	2	US-08-487-595-2	Sequence 2, Appli
40	128.5	6.4	252	2	US-08-414-657D-57	Sequence 57, Appli
41	128.5	6.4	287	2	US-08-414-657D-49	Sequence 49, Appli
42	128.5	6.4	310	2	US-08-414-657D-45	Sequence 45, Appli
43	128.5	6.4	315	2	US-08-414-657D-47	Sequence 47, Appli
44	128.5	6.4	338	2	US-08-414-657D-42	Sequence 42, Appli
45	128.5	6.4	338	2	US-08-414-657D-43	Sequence 43, Appli

ALIGNMENTS

RESULT 1
US-08-979-424-1
; Sequence 1, Application US/08979424
; Patent No. 5942606
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,424
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0405 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGFET03
CLONE: 1232054
US-08-979-424-1

Query Match 100.0%; Score 2012; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 3.7e-168;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MISLPGPLVNLRLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVLLPAMVTLHGEV 60
1 MISLPGPLVNLRLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVLLPAMVTLHGEV 60
61 SSSQPEVFPVMMFEPKQEKEDQVLSYINGVTTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
61 SSSQPEVFPVMMFEPKQEKEDQVLSYINGVTTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
61 SSSQPEVFPVMMFEPKQEKEDQVLSYINGVTTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
121 SGPYSCSVNVQDKGSKRGHSIKTLELNVLVPPAPPSCRLOGVPHVGANVTLSCOSPRSK 180
121 SGPYSCSVNVQDKGSKRGHSIKTLELNVLVPPAPPSCRLOGVPHVGANVTLSCOSPRSK 180
121 SGPYSCSVNVQDKGSKRGHSIKTLELNVLVPPAPPSCRLOGVPHVGANVTLSCOSPRSK 180
181 PAVOYQWDRQLPSFQTFFAFPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLE 240
181 PAVOYQWDRQLPSFQTFFAFPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLE 240
181 PAVOYQWDRQLPSFQTFFAFPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLE 240
241 VSTGPGAANVAGAVGTIVGLGLAGLVLLYHRRKALEBPANDIKEDATAIRTLPMWPKS 300
241 VSTGPGAANVAGAVGTIVGLGLAGLVLLYHRRKALEBPANDIKEDATAIRTLPMWPKS 300
241 VSTGPGAANVAGAVGTIVGLGLAGLVLLYHRRKALEBPANDIKEDATAIRTLPMWPKS 300
301 SDTISKNGTSSVTSARALRPPHGPBRPGALTPTPSLSSQALPSPRLPTTDGAHPQIPSP 360
301 SDTISKNGTSSVTSARALRPPHGPBRPGALTPTPSLSSQALPSPRLPTTDGAHPQIPSP 360
301 SDTISKNGTSSVTSARALRPPHGPBRPGALTPTPSLSSQALPSPRLPTTDGAHPQIPSP 360

QY 361 IPGVSSSSGLSRMGAVPMVPAQSQAGSLV 390
Db 361 IPGVSSSSGLSRMGAVPMVPAQSQAGSLV 390

RESULT 2

US-08-928-383B-26

; Sequence 26, Application US/08928383B

; Patent No. 6210921

; GENERAL INFORMATION:

; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,

; APPLICANT: and Marshall S. Horwitz

; TITLE OF INVENTION: CAR, A No. 6210921e1 Coxsackievirus and Adenovirus

; TITLE OF INVENTION: Receptor

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; FILING DATE: 12-SEP-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/026,100

; FILING DATE: 13-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: DFN-020

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 742-4214

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 365 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-928-383B-26

Query Match 17.6%; Score 353.5; DB 4; Length 365;
Best Local Similarity 27.8%; Pred. No. 4.7e-23;

Matches 113; Conservative 71; Mismatches 156; Indels 67; Gaps 15;

QY 9 VTNLRFPLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVLLPAMVTLHGEVSSQPE 67
Db 1 MARLLCFVLLCGIADFT---SGLSITTPQRIEAKAGETAYLLPCKFTLSPE--DGGPLD 54

```

QY 68 VPFVWMPFKQKEKE--DQVUSYINGVTTSKPGVSLVY-----SMPSRNL 109
      : | : | | : | : |
Db 55 IE--WLISPSDNQIVDQVILLYSG-----DKIYDNYYPDLKGRVHFTSNDVKS GDA 103

QY 110 SLRLBGLQEKDGPYSCSVNVQDKQKSRGHSIKTLELNVLPAPPPSCRLQGVPHVGAN 169
      : : | | | | | : | : | | | | : | : | : | : |
Db 104 SINVTNLQSLDIGTYQCKVK-----KAPGVANKKFLTLVLVKPSGTRCFYDGSSEI GND 157

QY 170 VTLSCOSPRKRPAYQYQWDQQLPSFQTFAPAL-DVIRGSLSTNLSSSMAGVYVC KAHN 228
      | | : : | : | : | : | : | : | : | : | : |
Db 158 FKIKCEPKEGSLPLQPEW-QKLSDSQTMPTPWLAEMTSPVLSVKNASSEYSGTYSC T VQ N 216

QY 229 EVGTAQCNTVLE-VSTGPGAAVVAGAVGTLVGLLGLVLYHRR--GKALEEPAND 284
      | | : | | : | : | | | | | : | : | : | : | : |
Db 217 RVGSDQCMRLDVPVPPSNRAGTIAGAVIGTLALVLIGAILFCCHRRKREKYEKEV HND 276

QY 285 IKEDAIAPRTLPMPKSSDTISKNGTLLSVTSARALRPHGPPRPGALTPTPSSL SQALPS 344
      | : | | : | | | : : : | : : | : : | : : | :
Db 277 IRED-----VPPPKSRTSTARSYIGSNHSSL-----GSMSPSNMEGYSK TQY 318

QY 345 PRLPTTDGAH-PQIISPPIPGGVSSGSLSRMGAVPVVWPAOSQAGSLV 390
      : : | : | : | : | : | : | : | : | : | : | : |
Db 319 NQVPSEDFERAPQSPPLAPAKVAPNLSRMGAVPVMI PAOSKDGSLV 365

```

Search completed: August 19, 2002, 17:09:51
Job time: 3219 sec

OM protein - protein search, using sw model

Run on: August 19, 2002, 16:21:32 ; Search time 42.75 Seconds
(without alignments)

876.604 Million cell

updates/sec

Title: US-09-902-759-39

Perfect score: 2012

Sequence: 1 MSLPGLVTNLLRFLFLGL.....SRMGAVPMVPAQSQAGSLV 390

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176	8.7	299	2 S56749	junctional adhesio
2	162.5	8.1	344	2 A27681	nonspecific cross-
3	158.5	7.9	847	2 JH0371	B-cell adhesion pr
4	155.5	7.7	3707	2 S18252	heparan sulfate pr
5	154.5	7.7	4391	2 A38096	perlecan precursor
6	153.5	7.6	647	2 A35648	B-cell adhesion pr
7	153.5	7.6	1040	2 A49356	transient axonal
8	152.5	7.6	521	2 S34338	biliary glycoprote
9	152	7.6	483	2 T17346	hypothetical prote
10	151.5	7.5	1036	2 S22383	axonin 1 precursor
11	151.5	7.5	4162	2 T42633	connectin/titin -
12	150.5	7.5	521	2 JCI508	biliary glycoprote

axonal glycoprotei
CD22 homolog/B lym
biliary glycoprote
hypothetical prote
hemiscetin precurs
carcinoembryonic

differentiation an
carcinoembryonic

13	150.5	7.5	1040	2 A34695	titin, cardiac mus
14	150	7.5	868	2 A46512	biliary glycoprote
15	149.5	7.4	341	2 JCI512	biliary glycoprote
16	147	7.3	5175	2 T20992	pregnancy-specific
17	147	7.3	5198	2 T43290	connectin 3B - chi
18	144	7.2	349	2 A34815	biliary glycoprote
19	143	7.1	862	2 I49583	pregnancy-specific
20	142	7.1	278	2 A39037	elastic titin - hu
21	141.5	7.0	26926	1 I38344	poliovirus recepto
22	141	7.0	458	2 JCI509	pregnancy-specific
23	139	6.9	458	1 WMM5R1	pregnancy-specific
24	138.5	6.9	495	2 A55181	pregnancy-specific
25	138.5	6.9	1323	2 P80568	pregnancy-specific
26	138	6.9	278	2 JCI506	pregnancy-specific
27	138	6.9	419	2 B54312	pregnancy-specific
28	137	6.8	7962	2 I38346	pregnancy-specific
29	136.5	6.8	518	2 JC4024	pregnancy-specific
30	135.5	6.7	426	2 C55181	pregnancy-specific
31	135.5	6.7	426	2 B35334	pregnancy-specific
32	135	6.7	428	2 J50032	pregnancy-specific
33	135	6.7	428	2 I57486	pregnancy-specific
34	134	6.7	240	2 JC4121	pregnancy-specific
35	134	6.7	436	2 B55181	pregnancy-specific
36	133	6.6	321	2 JH0395	biliary glycoprote
37	133	6.6	351	2 JH0396	biliary glycoprote
38	133	6.6	417	2 JH0394	biliary glycoprote
39	133	6.6	419	2 A36109	pregnancy-specific
40	133	6.6	464	2 C30127	transmembrane carc
41	133	6.6	526	1 A32164	biliary glycoprote
42	133	6.6	702	2 A36319	carcinoembryonic
43	132.5	6.6	166	2 A33402	pregnancy-specific
44	132.5	6.6	338	2 JC4776	limbic-system-asso
45	132.5	6.6	338	2 JCI238	opioid-binding pro

ALIGNMENTS

RESULT	1
S56749	junctional adhesion molecule precursor - human platelet F11 receptor
N,Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1;	
C,Species: Homo sapiens (man)	
C,Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002	
C,Accession: A59406; S56749	
R,Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.;	
Iwamatsu, A.; Kita, T.	
J. Immunol. 163, 553-557, 1999	
A,Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribution of junctional adhesion molecule in human endothelial cells.	
A,Reference number: A59406; MUID:99323940; PMID:10395639	
A,Accession: A59406	
A,Status: preliminary	
A,Molecule type: DNA	

A;Residues: 1-299 <OZA>
 A;Cross-references: GB:AAD42050; NID:g5326797; PIDN:AAD42050.1
 R;Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.
 Biochem. J. 310, 155-162, 1995
 A;Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a novel platelet receptor for monoclonal antibody F11 with the Fc-gamma-RII receptor.
 A;Reference number: S56749; MUID:95374438; PMID:7646439
 A;Accession: S56749
 A;Molecule type: protein
 A :
 28-49, 'X', 51-53, 62-73, 'E', 75-103, 123, 'F', 125-130, 'FDKDXITLYNXX', 'LT', 206, 'X', 208, 'Q' <NAI>
 A;Note: the order of the peptides other than the amino terminus was not determined
 C;Genetics:
 A;Gene: JAM
 C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane
 F;1-25/Domain: signal sequence #status predicted <SIG>
 F;26-299/Product: junctional adhesion molecule #status predicted <MAT>

Query Match 8.7%; Score 176; DB 2; Length 299;
 Best Local Similarity 25.7%; Pred. No. 0.00014;
 Matches 71; Conservative 46; Mismatches 129; Indels 30; Gaps 12;

QY 9 VTNLRLFLGLSALAPPSRAQLQLHPANRLQAVEGGEVVLPAWYTLHGEVSSQPMVEV 68
 | | | | : : : : | | : : | :
 Db 7 VERKLLCLFLIALCLSLALGSVTVHSSSEPEVRIPENNPVKLSCAYS-----GFSS 57
 QY 69 PFVMMFFKQKEKEDQVLSYINGVTTTSKPGVSLVYSMPSPRNLSLRLEGLOEKDGPYSCSV 128
 | | | | : : : : | | : : | : : : : : | : | : | :
 Db 58 PRVENKFDQGD-TTRLVCYNKKITASYE--DRVTFLLPT--GITFKSVTRDGTGTTCMV 111
 QY 129 NVQDKQKSRGHSIKTLELVNLPAPPSCRLLQGVPHVGAVNLTSCQSPRSKPAVOYOWD 188
 : : | | | : : : | | | | : : : : : : : : : : : : : : : :
 Db 112 S--EEGNSYG-EVK-VKLIIVLPSPSKPTVINIPSSAITGNRAVLITCSEQDGSPPSEYTFW 167
 QY 189 RQ---LP---SFQTF--FAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQ-CNVT 238
 : : | : | : : : | : | : | : | : | : | : | : | : | : | :
 Db 168 KDGIWPTNPKSTRAFSNSVYLNPTGELVFDPLASDTEGYSCARNGYGTPTMTSNAV 227
 QY 239 LEVSTGPGAAVVAGAVVGLVGLILA-GLVLLYHR 273
 : : : : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 228 RMEAVERNVGIYAAVLVTLILGLIVFGIWFAYS 263

Search completed: August 19, 2002, 17:10:57
 Job time: 2965 sec

OM protein - protein search, using sw model

Run on: August 19, 2002, 17:11:02 ; Search time 24.06 Seconds
(without alignments)

updates/sec 627.624 Million cell

Title: US-09-902-759-39

Perfect score: 2012

Sequence: 1 MISTPLGPIVTLIRFLFLGL.....SRMGAVPMVPAQSQAGSLV 390

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	353.5	17.6	365	1 CXAR_MOUSE	P97792 mus musculu
2	343	17.0	365	1 CXAR_HUMAN	P78310 homo sapien
3	297	14.8	319	1 A33_HUMAN	Q99795 homo sapien
4	212	10.5	298	1 JAM2_HUMAN	P57087 homo sapien
5	176	8.7	299	1 JAM1_HUMAN	Q9y624 homo sapien
6	168.5	8.4	300	1 JAM1_MOUSE	O88792 mus musculu
7	167.5	8.3	298	1 JAM1_BOVIN	Q9xt56 bos taurus
8	163	8.1	344	1 CEA6_HUMAN	P40199 homo sapien
9	158.5	7.9	4393	1 PGBM_HUMAN	P98160 homo sapien
10	155.5	7.7	3707	1 PGBM_MOUSE	Q05793 mus musculu
11	153.5	7.6	847	1 CD22_HUMAN	P20273 homo sapien
12	153.5	7.6	1040	1 AXOI_HUMAN	Q02246 homo sapien
13	151.5	7.5	1036	1 AXOI_CHICK	P26685 gallus gall
14	150.5	7.5	521	1 CEAL_MOUSE	P31809 mus musculu
15	150.5	7.5	1040	1 AXOI_RAT	P22063 rattus norv
16	146	7.3	515	1 PVRI_PIG	Q9g176 sus scrofa
17	145	7.2	517	1 PVRI_HUMAN	Q15223 homo sapien

18	144	7.2	349	1 CEA8_HUMAN	P31997 homo sapien
19	143	7.1	862	1 CD22_MOUSE	P35329 mus musculu
20	142.5	7.1	1709	1 SN_HUMAN	Q9bzz2 homo sapien
21	138.5	6.9	515	1 PVRI_MOUSE	Q9jxf6 mus musculu
22	138	6.9	348	1 KILQ_RAT	Q9z038 rattus norv
23	138	6.9	419	1 PSG4_HUMAN	Q00888 homo sapien
24	135.5	6.7	426	1 PSGB_HUMAN	Q00887 homo sapien
25	135	6.7	428	1 PSG3_HUMAN	Q16557 homo sapien
26	134.5	6.7	337	1 G55A_CHICK	Q98892 gallus gall
27	133	6.6	526	1 CEAL_HUMAN	P13688 homo sapien
28	133	6.6	702	1 CEA5_HUMAN	P06731 homo sapien
29	132.5	6.6	338	1 LAMP_HUMAN	Q13449 homo sapien
30	132.5	6.6	345	1 OPCM_HUMAN	Q14982 homo sapien
31	132.5	6.6	345	1 OPCM_RAT	P32736 rattus norv
32	132	6.6	252	1 CEA3_HUMAN	P40198 homo sapien
33	131.5	6.5	349	1 IACH_SCHAM	Q26474 schistocerc
34	131.5	6.5	538	1 PVRI_HUMAN	Q92692 homo sapien
35	131	6.5	519	1 ECTO_RAT	P16573 rattus norv
36	130.5	6.5	837	1 NCM2_MOUSE	O35136 mus musculu
37	130	6.5	761	1 NCA2_HUMAN	P13592 homo sapien
38	130	6.5	917	1 ICA5_MOUSE	Q60625 mus musculu
39	129.5	6.4	345	1 OPCM_BOVIN	P11834 bos taurus
40	128.5	6.4	338	1 LAMP_RAT	Q62813 rattus norv
41	128.5	6.4	837	1 NCM2_HUMAN	O15394 homo sapien
42	128	6.4	338	1 LAMP_CHICK	Q98919 gallus gall
43	128	6.4	530	1 PVRI_MOUSE	P32507 mus musculu
44	126.5	6.3	404	1 RAGE_HUMAN	Q15109 homo sapien
45	126	6.3	335	1 PSG5_HUMAN	Q15238 homo sapien

ALIGNMENTS

RESULT	ID	SEQUENCE	STANDARD;	PRT;	AA.
1	CXAR_MOUSE	P97792; 009052;			
CXAR_MOUSE	AC	30-MAY-2000 (Rel. 39, Created)			
	DT	30-MAY-2000 (Rel. 39, Last sequence update)			
	DT	01-MAR-2002 (Rel. 41, Last annotation update)			
	DE	Coxsackievirus and adenovirus receptor homolog precursor (mCAR).			
	GN	CXADR OR CAR.			
	OS	Mus musculus (Mouse).			
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
	OX	NCBI_TaxID=10090;			
	RN	[1]			
	RP	SEQUENCE FROM N.A.			
	RC	STRAIN=C57BL/6J; TISSUE=liver;			
	RX	MEDLINE=97190109; PubMed=9036860;			
	RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,			
	RA	Krishnas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;			
	RT	"Isolation of a common receptor for Coxsackie B viruses and			
	RT	adenoviruses 2 and 5."			
	RL	Science 275:1320-1323(1997).			
	RN	[2]			
	RP	SEQUENCE FROM N.A.			
	RC	STRAIN=C3H/MAI;			

OM protein - protein search, using sw model

Run on: August 19, 2002, 17:09:12 ; Search time 67.26 Seconds
(without alignments)

updates/sec 1003.093 Million cell

Title: US-09-902-759-39

Perfect score: 2012

Sequence: 1 MISTLPGBLVTNLRFLFLGL.....SRMGAVPMVPAQSQAGSLV 390

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description

1	2012	100.0	390	4	Q96AP7	Q96ap7 homo sapien
2	2009	99.9	390	4	Q96RS0	Q96t50 homo sapien
3	1931	96.0	390	6	Q95KI3	Q95ki3 macaca faec
4	1397	69.4	394	11	Q925F2	Q925f2 mus musculu
5	641.5	31.9	204	11	Q9D7I2	Q9d7i2 mus musculu
6	343	17.0	366	11	Q9DBJ8	Q9dbj8 mus musculu
7	341.5	17.0	372	13	Q90Y50	Q90y50 brachydanio
8	330	16.4	358	11	Q9R066	Q9r066 rattus norv
9	324.5	16.1	327	4	Q96IQ7	Q96iq7 homo sapien
10	320.5	15.9	325	4	Q95791	Q95791 homo sapien
11	316	15.7	407	11	Q9D2J4	Q9d2j4 mus musculu
12	307.5	15.3	373	4	Q9H6B4	Q9h6b4 homo sapien
13	290	14.4	284	4	Q9NX42	Q9nx42 homo sapien
14	287	14.3	373	11	Q920S5	Q920s5 mus musculu
15	279.5	13.9	318	13	Q91664	Q91664 xenopus lae
16	277.5	13.8	300	11	Q9D9J0	Q9d9j0 mus musculu
17	276.5	13.7	300	11	Q9DA22	Q9da22 mus musculu
18	272	13.5	352	11	Q91W66	Q91w66 mus musculu
19	269	13.4	304	11	Q9CVA4	Q9cva4 mus musculu
20	267.5	13.3	328	11	Q9Z109	Q9z109 mus musculu
21	267.5	13.3	344	11	Q9R067	Q9r067 rattus norv
22	266	13.2	335	13	Q9PWR4	Q9pwr4 gallus gall
23	264.5	13.1	344	4	Q9UKV4	Q9ukv4 homo sapien
24	263	13.1	335	13	Q9YGH1	Q9ygh1 gallus gall
25	262.5	13.0	259	4	Q95532	Q95532 homo sapien
26	259	12.9	319	11	Q922D5	Q922d5 mus musculu
27	258	12.8	319	6	Q9TU80	Q9tu80 canis fami
28	258	12.8	319	11	Q9UKA5	Q9jka5 mus musculu
29	257	12.8	248	11	Q9D0T4	Q9d0t4 mus musculu
30	256	12.7	319	6	Q9TU79	Q9tu79 sus scrofa
31	253	12.6	335	13	Q9YGV5	Q9ygv5 gallus gall
32	221	11.0	181	13	Q91665	Q91665 xenopus lae
33	196	9.7	577	11	Q9D2Z1	Q9d2z1 mus musculu
34	186.5	9.3	977	4	Q96RD9	Q96rd9 homo sapien
35	183	9.1	300	11	Q9JHY1	Q9jhy1 rattus norv
36	176	8.7	298	11	Q9UI59	Q9ji59 mus musculu
37	171	8.5	381	4	Q9Y4A4	Q9y4a4 homo sapien
38	169.5	8.4	309	4	Q96FL1	Q96fl1 homo sapien
39	169.5	8.4	310	4	Q9BX67	Q9bx67 homo sapien
40	168.5	8.4	430	4	Q15600	Q15600 homo sapien
41	166.5	8.3	310	11	Q9D8B7	Q9d8b7 mus musculu
42	166	8.3	310	11	Q9EPK4	Q9epk4 mus musculu
43	166	8.3	310	11	Q9D1M9	Q9dlm9 mus musculu
44	164	8.2	538	4	Q9NWQ7	Q9nwg7 homo sapien
45	163.5	8.1	512	4	Q96DN8	Q96dn8 homo sapien

ALIGNMENTS

RESULT 1
Q96AP7
ID Q96AP7 PRELIMINARY; PRT; 390 AA.
AC Q96AP7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 41.2 KDA PROTEIN.

Query Match	100.0%;	Score 2012;	DB 4;	Length 390;
Best Local Similarity	100.0%;	Pred. No. 9.6e-156;		
Matches 390;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

RESULT	2	
ID	Q96T50	PRELIMINARY; PRT; 390 AA.
AC	Q96T50;	
DT	01-DEC-2001	(TREMBLrel. 19, Created)
DT	01-DEC-2001	(TREMBLrel. 19, last sequence update)
DT	01-DEC-2001	(TREMBLrel. 19, last annotation update)
DE	ENDOTHELIAL CELL-SELECTIVE ADHESION MOLECULE.	
GN	ESAM.	
OS	Homo sapiens (Human).	

Query Match	99.9%	Score 2009;	DB 4;	Length 390;
Best Local Similarity	99.7%	Pred. No. 1.7e-155;		
Matches 389; Conservative	1;	Mismatches 0;	Indels 0;	Gaps

RESULT	3	
095K13		
ID	095K13	PRELIMINARY;
AC	095K13;	PRT; 390 AA.
DT	01-DEC-2001	(TREMBLrel. 19, Created)
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)
DE	HYPOTHETICAL 40.9 KDA PROTEIN.	
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).	

DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE 231008D05RIK PROTEIN.
GN ESAM OR 231008D05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Aeburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK009223; BAB26146.1; -.
DR MGD; MGI:1916774; Esam.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; Ig_like; 1.
SQ SEQUENCE 204 AA; 22352 MW; 021B29BE2B05F494 CRC64;

Query Match 31.9%; Score 641.5; DB 11; Length 204;
Best Local Similarity 66.2%; Pred. No. 1.5e-44;
Matches 129; Conservative 25; Mismatches 38; Indels 3; Gaps 2;

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DB 1 MILQAGTPETSLRLVFLGLSTLAAPSPRAQLQLHP--ANRLQAVEGSEVVLPAWYTLHG 60
QY 59 EVSSSQPWEVFPVWPFKQKEKE-DVLSYINGVTTSKPGVSLVYMSRNLISRLGLQ 117
DB 61 EESWSPREVPILWFLFLEQEGKEPNQVLSYINGVMTNKKPGTALVHSSIRNVSRLGLAQ 120
QY 118 EKDSGPYSCSVNVQDKQKSGHSIKTLELNVLPAPAPSCSLQGVPHVGANVTLSQSP 177

DB 121 EGDSTYRCVNVQNDCKSGHSIGHSIKSLKVLVPPAPPPSCSLQGVPHVGANVTLSQSP 180
QY 178 RSKPAVQYQWDRQLP 192
DB 181 RSKPTAQYQWERTAP 195
Search completed: August 19, 2002, 17:15:52
Job time: 400 sec

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:01:07 ; Search time 2294.29 Seconds
(without alignments)
updates/sec 16536.624 Million cell

Title: US-09-902-759-38
Perfect score: 1813
Sequence: 1 ggagccgccttggtgtccag.....cataatgtttgtatgaaaaa 1813

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_hcgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1813	100.0	1813	6	AX076924 Sequence
2	1809.8	99.8	1838	9	AF361746 Homo sapi
3	1809	99.8	1821	6	AX136161 Sequence
4	1804.8	99.5	1816	6	AX191598 Sequence
5	1760.4	97.1	1831	6	AX073678 Sequence
6	1691.8	93.3	1734	9	BC016868 Homo sapi
7	1659.6	91.5	1855	9	AB060855 Macaca fa
8	1171.4	64.6	1173	6	AX191588 Sequence
9	861.6	47.5	1840	10	AF361882 Mus muscu
10	828.2	45.7	187960	9	AP000866 Homo sapi
11	793.2	43.8	101458	2	AP000680 Homo sapi
12	717.4	39.6	736	9	AF272292 Homo sapi
13	531.2	29.3	637	6	AX136493 Sequence
14	453	25.0	541	6	AX136640 Sequence
15	441	24.3	441	6	AX332845 Sequence
16	339	18.7	221961	10	AC073435 Mus muscu
17	323.8	17.9	340	6	AX331694 Sequence
18	323.8	17.9	340	6	AX333904 Sequence
19	183.2	10.1	81318	2	AC016125 Homo sapi
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21	162	8.9	187960	9	AP000866 Homo sapi
22	132.8	7.3	637	9	HSB326182 Homo sapi
23	132.8	7.3	674	9	HSB329044 Homo sapi
24	120	6.6	698	9	HSB331517 Homo sapi
25	79.8	4.4	46240	2	AC105958 Mus muscu
26	75	4.1	81318	2	AC016125 Homo sapi
27	71	3.9	674	9	HSB331520 Homo sapi
28	70.8	3.9	125020	9	AF429315 Homo sapi
29	70	3.9	611	9	HSB323034 Homo sapi
30	59.6	3.3	165556	2	AC087190 Homo sapi
31	58.2	3.2	1147	9	BC007313 Homo sapi
32	58.2	3.2	1161	6	AX056679 Sequence
33	58.2	3.2	1221	9	AK000460 Homo sapi
34	58	3.2	125020	9	AF429315 Homo sapi
35	54.2	3.0	95209	2	AP004323 Oryza sat
36	54.2	3.0	153292	2	AP003635 Oryza sat
37	51.4	2.8	7218	6	I66494 Sequence 14
38	51	2.8	51	6	AX161199 Sequence
39	51	2.8	51	6	AX161201 Sequence
40	50.4	2.8	57245	2	AC068263 Homo sapi
41	50	2.8	50	6	AX076928 Sequence
42	49.6	2.7	144973	2	AC096689 Oryza sat

C 43 49.4 2.7 51 6 AX161200 Sequence
C 44 49 2.7 1614 6 AX239602 Sequence
C 45 49 2.7 12425 6 AX239607 Sequence

ALIGNMENTS

RESULT 1
AX076924 1813 bp DNA linear PAT

LOCUS AX076924 1813 bp DNA linear PAT

22-FEB-2001

DEFINITION Sequence 36 from Patent WO0105836.

AX076924

VERSION AX076924.1 GI:13121579

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1813)

AUTHORS Botstein,D., Goddard,A., Gurney,A.L., Hillan,K.J., Roy,M.A. and

Wood,W.I.

TITLE Polypeptidic compositions and methods for the treatment of tumors

JOURNAL Patent: WO 0105836-A 36 25-JAN-2001;

Genentech, Inc. (US)

FEATURES Location/Qualifiers

source 1..1813

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 368 a 559 c 484 g 402 t

ORIGIN

Query Match 100.0%; Score 1813; DB 6; Length 1813;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps

0;

QY 1 ggagccgcccgtggtcagcgctcgctcccgcgacgctccggcgtcgcgacgct 60

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Db 61 CGGCACTGCAGAGTCCGTGCTGCCGCGGCTGCGCCCTGACTCCGCTCCGCGCAGGA 120

QY 121 gggccatgattccctccgggggccccctggtgacccaactgtcggttttgcctcg 180

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QY 181 ggtcagtgccctcgccccccctcgcgcccaagtgcgaactgcacttgcccgccaacc 240

Db 181 GGCTAGTGCCTCGGCCCCCTGCGGCGGCGCACTGCACTTGCCCGCCAACC 240

QY 241 ggtcagtgccctcgccccccctcgcgcccaagtgcgaactgcacttgcccgccaacc 300

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QY 301 aggtcttcaccccgccatgggagggtgcccttgtgatgtggtcttcaacagaag 360

Db 301 AGGTGCTTCATCCCGACCATGGAGGTGCCCTTGTGATGTGTCTTCAACAGAAAG 360

QY 361 aaaaggagatcaggtgtgtcctacatcaatggggcacaacaagcaactcggagat 420

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QY 1261 tggctgctgcccagagtgcaagctggtctctctgtatgatgaccccaaccatctgtcta 1320

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QY 1801 ttgtatgaaaaa 1813

Db 1801 TTTGTATGAAAAA 1813

RESULT 2

AF361746 AF361746 1838 bp mRNA linear PRI

LOCUS 07-MAY-2001

DEFINITION Homo sapiens endothelial cell-selective adhesion molecule (ESAM)

ACCESSION AF361746

VERSION AF361746.1 GI:13959017

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

AUTHORS Hirata,K.-I., Ishida,T., Penta,K., Rezaee,M., Yang,E., Wohlgemuth,J. and Quettermous,T.

TITLE Cloning of an Immunoglobulin Family Adhesion Molecule Selectively Expressed by Endothelial Cells

JOURNAL J. Biol. Chem. 276 (19), 16223-16231 (2001)

PUBMED 11279107

REFERENCE 2 (bases 1 to 1838)

AUTHORS Quettermous,T., Ishida,T. and Hirata,K.-I.

TITLE Direct Submission

JOURNAL Submitted (15-MAR-2001) Cardiovascular Medicine, Stanford University, 300 Pasteur Drive, Falk CVRC, Stanford, CA 94305-5406, USA

FEATURES

source location/qualifiers

1..1838

/organism="Homo sapiens"

/db_xref="taxon:9606"

1..1838

/gene="ESAM"

139..1311

/gene="ESAM"

/note="immunoglobulin superfamily; contains V and C2 domains"

/codon_start=1

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/protein_id="AAK51065.1"

/db_xref="GI:13959018"

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ORIGIN

Query Match 99.8%; Score 1809.8; DB 9; Length 1838;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1811; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 cggcacctgcaggtcagtgctcctcccgcggtcgccctgagctccgctccggcagagga 120

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QY 121 ggscatgatctccctcccgggggccctgtgacacaactgtctgggttttctctctg 180

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RESULT 3

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LOCUS AX136161 1821 bp DNA linear PAT
30-MAY-2001
DEFINITION Sequence 83 from Patent EP1067182.
ACCESSION AX136161
VERSION AX136161.1 GI:14272569
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 1821)
Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE
Secretory protein or membrane protein
JOURNAL
Patent: EP 1067182-A 83 10-JAN-2001;
Helix Research Institute (JP)
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1. 1821
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15-AUG-2001
DEFINITION Sequence 120 from Patent WO0149728.
ACCESSION AX191598
VERSION AX191598.1 GI:15209789

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1816)
AUTHORS Kato, S. and Kimura, T.
TITLE Human proteins having hydrophobic domains and dnas encoding these proteins
JOURNAL Patent: WO 0149728-A 120 12-JUL-2001;
FEATURES
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AX073678
LOCUS AX073678 1831 bp DNA linear PAT
06-FEB-2001
DEFINITION Sequence 12 from Patent WO0104264.
ACCESSION AX073678
VERSION AX073678.1 GI:12710099
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1831)

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ACCESSION BC016868
VERSION BC016868.1 GI:16877212
KEYWORDS MGC.
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1734)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA
94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxl.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

found
Clone distribution: MGC clone distribution information can be
through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
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13-JUN-2001
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sequence.
ACCESSION AB060855
VERSION AB060855.1 GI:13874503
KEYWORDS oligo capping, fis (full insert sequence).
SOURCE Macaca fascicularis adult male temporal lobe right cDNA to mRNA,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.
REFERENCE 1 (sites)
AUTHORS Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
Terano,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
TITLE Isolation of full-length cDNA clones from macaque brain cDNA
libraries
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1855)
AUTHORS Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.

' TITLE Direct Submission
JOURNAL Submitted (27-APR-2001) Katayuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E - m a i l : k h a s h i @ n i h . g o . j p ,
URL: http://www.nih.go.jp/yoiken/genbank/,
Tel: 81-3-5285-1111 (ex. 2120), Fax: 81-3-5285-1181)

COMMENT
Lab host: TOP10
Vector: PME18S-FL3 (Acc.No. AB009864)
R. Site1: DraIII (CACTGTGTG)
R. Site2: DraIII (CACCATGTG)
Description: 1st strand cDNA was primed with an oligo(dT) primer [ATGCGCCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct DraIII sites of PME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert.

Libraries
were constructed by oligo-capping method (Sugano et al., , Institute of Medical Science, University of Tokyo).
Custom primer used for sequencing
(5' end primer [CTTCTGCTCTAAAGTCGCG];
3' end primer [CGACCTCGAGCTCGAGCACAC]).

FEATURES
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ORIGIN

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LOCUS AX191588 1173 bp DNA linear PAT
15-AUG-2001

DEFINITION Sequence 110 from Patent WO0149728.

ACCESSION AX191588

VERSION AX191588.1 GI:15209770

KEYWORDS

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1173)

AUTHORS

Kato,S. and Kimura,T.

Human proteins having hydrophobic domains and dnas encoding these

proteins

JOURNAL Patent: WO 0149728-A 110 12-JUL-2001;

Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)

FEATURES

source location/Qualifiers

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Best Local Similarity 99.9%; Pred. No. 2.1e-261;

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 LOCUS AF361882 1840 bp mRNA linear ROD
 08-MAY-2001
 DEFINITION Mus musculus endothelial cell-selective adhesion molecule (Esam)
 mRNA, complete cds.
 ACCESSION AF361882
 VERSION AF361882.1 GI:13991772
 KEYWORDS
 SOURCE house mouse.
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Mus.
 REFERENCE 1 (bases 1 to 1840)
 AUTHORS Hirata, K.-I., Ishida, T., Penta, K., Rezaee, M., Yang, E.,
 Wohlgemuth, J., and Quertermous, T.
 TITLE Cloning of an immunoglobulin family adhesion molecule selectively
 expressed by endothelial cells
 JOURNAL J. Biol. Chem. 276 (19), 16223-16231 (2001)
 PUBMED 11279107
 REFERENCE 2 (bases 1 to 1840)
 AUTHORS Quertermous, T., Ishida, T. and Hirata, K.-I.
 TITLE Direct Submission
 JOURNAL Submitted (16-MAR-2001) Cardiovascular Medicine, Stanford
 University, 300 Pasteur Drive, Falk CVRC, Stanford, CA
 94305-5406, USA
 FEATURES Location/Qualifiers
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 /strain="Swiss Webster/NIH"
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 gene 1..1840
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 CDS 118..1302
 /gene="Esam"
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 immunoglobulin superfamily"
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 /protein_id="AAK51504.1"
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 CSLQGVPPVGINVTLANCKSPRSKPTAOYQWERLAPSSQFFGPAIDAVGSLKLTNLS
 IMSGVYVCKAQNRRVGFAPKCNVTLDMVTGSKAAVAVAGVGTGVLVLAGVLVLYOR
 RSKTLEELANDIKEDALAPRTLPWTGSDTISKNGTSSVTSRALRPPKAPRPGR
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 LV"
 BASE COUNT 404 a 498 c 482 g 456 t
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Best Local Similarity		73.3%;	Pred. No. 1.9e-189;		
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Db	820	tttgccaagtccaaacgtgacttggaactgatatgacagggtccaaaggctgacgtgcgt 879			
Qy	879	ggagctgtgtgggtaccctggttggaactgggggtgtgctggtggctggtcctctgtac 938			
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Qy	1638	tctaaccacaaccttggctcc-cactccagctccctgtatgatataaactgtcaggctg 1696			
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Qy	1697	gcttggttaggttctactggggca-gaggatagggaatctcttatataaactaacatgaa 1755			
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DRAFT

SEQUENCE, 25 unordered pieces.

ACCESSION AP000680

VERSION AP000680.2 GI:8118868

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens DNA, clone:CMB9-25K9.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Homo sapiens 101,458 genomic DNA of 11q24

JOURNAL Published Only in Database (1999) In press

REFERENCE 2 (bases 1 to 101458)

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Direct Submission

JOURNAL Submitted (08-NOV-1999) Masahira Hattori, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)

On May 31, 2000 this sequence version replaced gi:6997554.

----- Genome Center

Center: RIKEN Genomic Sciences Center (GSC)

Center code: RIKEN

Web site: http://hgp.gsc.riken.go.jp/

Contact: hattori@gsc.riken.go.jp/

----- Project Information

Center project name: HumDraft11

Center clone name: CMB9-25K9

----- Summary Statistics

Sequencing vector: PCR products; 100% of reads

Chemistry: Dye-terminator ET-amersham; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 89733 bases at least Q40

Consensus quality: 95050 bases at least Q30

Consensus quality: 97741 bases at least Q20

Insert size: 99058; sum-of-contigs

Quality coverage: 4.65x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists

25 contigs. The true order of the pieces is not known and their

order in this sequence record is arbitrary. Gaps between the

contigs are represented as runs N, but the exact sizes of the

gaps

are unknown. This record will be updated with the finished

sequence

as soon as it is available and the accession number will be

preserved

1 9364 contig of 9364 bp in length

9465 16830 contig of 7366 bp in length

16931 23631 contig of 6701 bp in length

23732 29864 contig of 6133 bp in length

29965 38284 contig of 8320 bp in length

38385 44338 contig of 5954 bp in length

44339 44438: gap of 100 bp

44439 49484: contig of 5046 bp in length

49485 49584: gap of 100 bp

49585 55550: contig of 5966 bp in length

55551 55650: gap of 100 bp

55651 61139: contig of 5489 bp in length

61140 61239: gap of 100 bp

61240 65471: contig of 4232 bp in length

65472 65571: gap of 100 bp

65572 69042: contig of 3471 bp in length

69043 69142: gap of 100 bp

69143 73512: contig of 4370 bp in length

73513 73612: gap of 100 bp

73613 76146: contig of 2534 bp in length

76147 76246: gap of 100 bp

76247 79045: contig of 2799 bp in length

79046 79145: gap of 100 bp

Sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 25 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 9364: contig of 9364 bp in length

* 9365 9464: gap of 100 bp

* 9465 16830: contig of 7366 bp in length

* 16831 16930: gap of 100 bp

* 16931 23631: contig of 6701 bp in length

* 23632 23731: gap of 100 bp

* 23732 29864: contig of 6133 bp in length

* 29865 29964: gap of 100 bp

* 29965 38284: contig of 8320 bp in length

* 38285 38384: gap of 100 bp

* 38385 44338: contig of 5954 bp in length

* 44339 44438: gap of 100 bp

* 44439 49484: contig of 5046 bp in length

* 49485 49584: gap of 100 bp

* 49585 55550: contig of 5966 bp in length

* 55551 55650: gap of 100 bp

* 55651 61139: contig of 5489 bp in length

* 61140 61239: gap of 100 bp

* 61240 65471: contig of 4232 bp in length

* 65472 65571: gap of 100 bp

* 65572 69042: contig of 3471 bp in length

* 69043 69142: gap of 100 bp

* 69143 73512: contig of 4370 bp in length

* 73513 73612: gap of 100 bp

* 73613 76146: contig of 2534 bp in length

* 76147 76246: gap of 100 bp

* 76247 79045: contig of 2799 bp in length

* 79046 79145: gap of 100 bp

Db 541 GGCAGAGACTTCCAGTACTGAGTCTCCAGGCCCTTGAATCTGTACCCCAACCCTTATC 600
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LOCUS AX136493 637 bp DNA linear PAT
DEFINITION Sequence 415 from Patent EP1067182.
ACCESSION AX136493
VERSION AX136493.1 GI:14272897
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 415 10-JAN-2001;
Helix Research Institute (JP)

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QY 121 gggccatgatctccctccggggcccttgatgaaccaactgtcgggttttctcctgg 180
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QY 361 aaaagagagatcaggtgtgttctcatcaatggtgtcacaacagaacctggagrat 420
Db 372 AAAAGAGATCAGGTGTGTCTTACATCAATGGGGTCAACAAGCAAACTGGAGTAT 431

QY 421 ccttggtctactccatgccctcccggaacctgtccctgcggtgaggggtccagaga 480
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QY 481 aagactctgccccctacagctgtccg-tgaatgtgcaagacaac-aaggcaatctag 538
Db 492 AAAGACTCTGGCCCTACAGCTGCTCCGTTGAATGTGCAGACAAACAAAGCAATCTTA 551

QY 539 gggccaca--gcatacaaaccttagaactcaatgtactgtgtccctcagctccatcc 596
Db 552 GGCCACAGCATCAAAAACCTTANAACTCAATGTACTGTGTCTCCANCTNTCCATCC 611
QY 597 t 597
Db 612 T 612

RESULT 14
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LOCUS AX136640 541 bp DNA linear PAT
DEFINITION Sequence 562 from Patent EP1067182.
ACCESSION AX136640
VERSION AX136640.1 GI:14273044
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 562 10-JAN-2001;
Helix Research Institute (JP)

FEATURES
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/db_xref="taxon:9606"
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ORIGIN

QY 153 a 120 c 110 g 141 t 17 others
Db 153 a 120 c 110 g 141 t 17 others

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Best Local Similarity 91.8%; Pred. No. 1.3e-94;
Matches 490; Conservative 0; Mismatches 42; Indels 2; Gaps

2; '
QY 1277 tcaagctggctctctggtatgatgacccccaccactcattggctaaaggattgggtctc 1336
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QY 1337 tccctcctataagggtcacctctagcacagagggcctgagtcattgggaaagagtcacactc 1396
Db 475 TCCTTCTATAAGGGTCACTTTTAGCACAGAGCGCTGAGTCATGGGAAAGAGTCACACTTC 416
QY 1397 ctgaccttgtaactctgcccccaactctcttaactgtgsgaaaaccatctcagtaagac 1456
Db 415 NTGACCCTTAGTATTNCCCCCACTTTTNTANTGTGGAAAAACATNTCAGTAAGAC 356
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QY 1516 caccacccctgactcctccttatgaagccagctgctgaaattagctactcaccaagagt 1575
Db 295 CACCAACCCCTGATTCTTCCTTATGAAGCCAGCTGCTGAAATTAGCTANTCACAAGAGT 236
QY 1576 gaaggagcagaagactccagtcactgagtcctccaggcccccttgatctgtacccccccc 1635
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QY 1756 atatgtgtgttctcatcttgcaatttaataaagatatcaatgttgtatga 1809
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RESULT 15
AX332845 LOCUS AX332845 441 bp DNA linear PAT
09-JAN-2002 DEFINITION Sequence 3354 from Patent WO0194629.
AX332845 ACCESSION AX332845
VERSION AX332845.1 GI:18123479
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endreass,G.,
Horrigan,S., Soppe,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using
signature
JOURNAL Patent: WO 0194629-A 3354 13-DEC-2001;

FEATURES
Avalon Pharmaceuticals (US)
Location/Qualifiers
source 1..441
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 118 a 118 c 96 g 109 t
ORIGIN

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Db 61 CCCCACTCTCTTACTGTGGAAAAACCATCTGATAAGACTTAAGTGTCCAGAGACAG 120

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Db 181 TTATGAAGCCAGCTGCTGAAATTAGCTAATCAACCAAGAGTAGGGGACAGACTTCCAGT 240

QY 1596 cactgagtcctccaggcccccttgatctgtacccccctatactaaacacccctggc 1655
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Db 361 GGGCAGAGGATAGGGAATCTTATTAAACTAACATGAAATATGTGTTCATTG 420

QY 1776 caaatttaataaagatcacat 1796
Db 421 CAAATTTAAATAAAGATACAT 441

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(without alignments)
14122.616 Million cell updates/sec

Title: US-09-902-759-38
Perfect score: 1813
Sequence: 1 ggaagccgcctcggtgtcag.....cataatgtttgtatgaaaaa 1813

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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19: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1813	100.0	1813	20	AAK52221	Protein PRO246 cDN
2	1813	100.0	1813	20	AAK28436	EGF-like homologue
3	1813	100.0	1813	21	AAK30052	Human PRO246 nucle
4	1813	100.0	1813	22	AAK21412	Human cDNA sequenc
5	1813	100.0	1813	22	AAK60372	PRO246 coding sequ
6	1813	100.0	1813	22	AAK87040	Nucleotide sequenc
7	1813	100.0	1813	22	AAK72379	Human PRO246 cDNA.
8	1813	100.0	1813	22	AAK97441	Human angiogenesis
9	1809	99.8	1821	22	AAK93785	Human cDNA encodin
10	1806.6	99.6	1827	22	AAK02949	Human shear stress
11	1804.8	99.5	1816	22	AAK12605	Human protein havi
12	1802	99.4	1954	21	AAK23441	CDNA encoding huma
13	1783.8	98.4	1932	21	AAK265278	Human secreted pro
14	1760.4	97.1	1831	22	AAK85076	Atherosclerosis-as
15	1757.6	96.9	1869	22	AAK44978	Human INTERCEPT
16	1756	96.9	1869	22	AAK45014	Human secreted pro
17	1756	96.9	1869	22	AAK45015	Human secreted pro
18	1756	96.9	1869	22	AAK45016	Human secreted pro
19	1756	96.9	1869	22	AAK45017	Human secreted pro
20	1440.8	79.5	1748	22	ABA09181	Human viral recept
21	1440.8	79.5	1748	22	AAK59707	Human polynucleoti
22	1376	75.9	1387	20	AAK87000	Human viral recept
23	1083.2	59.7	1290	20	AAK200447	Human secreted pro
24	1069.8	59.0	1110	22	AAK44979	Human INTERCEPT
25	1066.2	58.9	1110	22	AAK45046	Human secreted pro
26	1068.2	58.9	1110	22	AAK45047	Human secreted pro
27	1068.2	58.9	1110	22	AAK45048	Human secreted pro
28	1068.2	58.9	1110	22	AAK45049	Human secreted pro
29	1010.4	55.7	1606	22	AAK57921	Human polynucleoti
30	863.2	47.6	1846	22	AAK45020	Murine secreted pr
31	861.6	47.5	1846	22	AAK44981	Murine INTERCEPT
32	861.6	47.5	1846	22	AAK45018	Murine secreted pr
33	861.6	47.5	1846	22	AAK45021	Murine secreted pr
34	860	47.4	1846	22	AAK45019	Murine secreted pr
35	730.2	40.3	1182	22	AAK45052	Murine secreted pr
36	728.6	40.2	1182	22	AAK44982	Murine INTERCEPT
37	728.6	40.2	1182	22	AAK45050	Murine secreted pr
38	728.6	40.2	1182	22	AAK45053	Murine secreted pr
39	727	40.1	1182	22	AAK45051	Murine secreted pr
40	578.4	31.9	1288	22	AAK10122	Mouse 10.3 kDa pro
41	531.2	29.3	637	22	AAK93981	Primer specific fo
42	453	25.0	541	22	AAK94128	Primer specific fo
43	251.2	14.2	571	22	AAK97944	Murine 7-transmemb
44	226.4	12.5	564	22	AAK97943	Murine 7-transmemb
45	208	11.5	533	22	AAK97945	Murine 7-transmemb

ALIGNMENTS

RESULT 1
AAK52221
ID AAK52221 standard; DNA; 1813 BP.

XX AAX52221;
AC
XX
DT 25-JUN-1999 (first entry)
XX
DE Protein PRO246 cDNA clone DNA35639-1172.
XX
KW Secreted protein; transmembrane protein; human; enterocolitis;
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW congenital microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
KW fibromodulin; dermal scarring; Usher Syndrome; Atrophla areata;
KW anti-thrombotic; wound healing; tissue repair; ss.
XX
OS Homo sapiens.
XX
PN W09914328-A2.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-US19330.
XX
PR 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059113.
PR 17-SEP-1997; 97US-0059115.
PR 17-SEP-1997; 97US-0059117.
PR 17-SEP-1997; 97US-0059119.
PR 17-SEP-1997; 97US-0059121.
PR 17-SEP-1997; 97US-0059122.
PR 17-SEP-1997; 97US-0059124.
PR 18-SEP-1997; 97US-0059263.
PR 18-SEP-1997; 97US-0059266.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062287.
PR 21-OCT-1997; 97US-0063486.
PR 24-OCT-1997; 97US-0062814.
PR 24-OCT-1997; 97US-0062816.
PR 24-OCT-1997; 97US-0063045.
PR 24-OCT-1997; 97US-0063120.
PR 24-OCT-1997; 97US-0063121.
PR 24-OCT-1997; 97US-0063127.
PR 24-OCT-1997; 97US-0063128.
PR 27-OCT-1997; 97US-0063329.
PR 27-OCT-1997; 97US-0063327.
PR 28-OCT-1997; 97US-0063541.
PR 28-OCT-1997; 97US-0063542.
PR 28-OCT-1997; 97US-0063544.
PR 28-OCT-1997; 97US-0063549.
PR 28-OCT-1997; 97US-0063550.
PR 28-OCT-1997; 97US-0063564.
PR 29-OCT-1997; 97US-0063435.
PR 29-OCT-1997; 97US-0063704.
PR 29-OCT-1997; 97US-0063732.
PR 29-OCT-1997; 97US-0063738.
PR 29-OCT-1997; 97US-0063734.
PR 29-OCT-1997; 97US-0064215.

PR 29-OCT-1997; 97US-0063735.
PR 31-OCT-1997; 97US-0063870.
PR 31-OCT-1997; 97US-0064103.
PR 03-NOV-1997; 97US-0064248.
PR 07-NOV-1997; 97US-0064809.
PR 12-NOV-1997; 97US-0065186.
PR 17-NOV-1997; 97US-0065846.
PR 18-NOV-1997; 97US-0065693.
PR 21-NOV-1997; 97US-0066120.
PR 21-NOV-1997; 97US-0066364.
PR 24-NOV-1997; 97US-0066772.
PR 24-NOV-1997; 97US-0066466.
PR 24-NOV-1997; 97US-0066770.
PR 24-NOV-1997; 97US-0066511.
PR 24-NOV-1997; 97US-0066453.
XX
XX
PA (GETH) GENENTECH INC.
XX
XX
PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
XX
XX WPI; 1999-229533/19.
DR
DR P-PSDB; AAY13351.
DR
XX
XX
PT New isolated human genes and polypeptides used in, e.g. treatment of
PT Gastrointestinal ulceration
XX
XX
PS Claim 2; Fig 16; 320pp; English.
XX
CC AAX52213-74 encode secreted and transmembrane human proteins, and are
CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
CC fetal brain, fetal liver and fetal retina. The encoded polypeptides
CC have specific uses based on their homology to known polypeptides,
CC e.g. PRO211 and PRO217 can be used for disorders associated with the
CC preservation and maintenance of gastrointestinal mucosa and the repair
CC of acute and chronic mucosal lesions (e.g. enterocolitis,
CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
CC microvillus atrophy), skin diseases associated with abnormal
CC keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as
CC lung squamous cell carcinoma of the vulva and gliomas), potent effects
on
CC cell growth and development, diseases related to growth or survival of
CC nerve cells including Parkinson's disease, Alzheimer's disease, ALS,
CC neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for
CC reducing dermal scarring. PRO264 can be used as a target for anti-tumor
CC drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophla
CC areata; PRO269 can be used as an anti-thrombotic agent; PRO287
CC polypeptides and portions may have therapeutic applications in wound
CC healing and tissue repair; PRO317 can be used for treating problems of
CC the kidney, uterus, endometrium, blood vessels, or related tissue, e.g.
in the heart of genital tract.
XX
SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 20; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	ggagccgcctgggtctcagcggctcggctcccgcgacgctccggcgtcggcgagcct	60	QY	901	ttggaactggggttgtcgtggctgtgtcctcttgtaaccaaccgcggggcaaggcccttg	960
QY	61	cggaacctgacaggtccgtgcgtcccgcggtcggcgcccttgaactccgtcccgacaggga	120	Db	901	ttggaactggggttgtcgtggctgtgtcctcttgtaaccaaccgcggggcaaggcccttg	960
Db	61	cggaacctgacaggtccgtgcgtcccgcggtcggcgcccttgaactccgtcccgacaggga	120	QY	961	aggagccagccaatgatatacaaggagatgccaattgtcccccgaacctgtccctggccca	1020
QY	121	gggccaatgatctccctccggggggccctctgttgaccaacttgctgcggtttttgttccctgg	180	Db	961	aggagccagccaatgatatacaaggagatgccaattgtcccccgaacctgtccctggccca	1020
Db	121	gggccaatgatctccctccggggggccctctgttgaccaacttgctgcggtttttgttccctgg	180	QY	1021	agagctcagacaacaatctccaagaatgggaaccttctcctctgtcaacctccgacgagccc	1080
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Db	181	ggctgaagtgccttcgcgccccctcgcggggcccaagtgcacaatgcaattgcccgcgaacc	240	QY	1081	tccggccaaccccatggccctcccaaggcctgtgtgcatggaaccccaacgcccagctctcca	1140
QY	241	ggctgcaggcggtggaagggggaagtgtgtctccagcgtgtgtaacacttgcacgggg	300	Db	1081	tccggccaaccccatggccctcccaaggcctgtgtgcatggaaccccaacgcccagctctcca	1140
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Db	601	gtctccaagggtgcccccatgtgggggcaaacgtgacccctgagctgcaggtctccaaggga	660	QY	1501	attgggaaggagcctccaaccccaacctgactcctcctatgaagcagagctgtgaaatag	1560
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Db	661	gtaagccgcgtgtccaataaccagtgggatcggcagcttccatccctccaagaacttctcttg	720	QY	1561	ctactcaaccaagaagtgaaggggcagagaactccagtcaactgagtctcccaaggcccttga	1620
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QY	781	ctggaagtctaagtctgcaagggccaacaatgagtgggcactgcccacaatgttaatgtgacgc	840	Db	1621	tctgtaccccccaacctatctaacaaccaacctgtgctcccaactccagctccctgtatgat	1680
Db	781	ctggaagtctaagtctgcaagggccaacaatgagtgggcactgcccacaatgttaatgtgacgc	840	QY	1681	ataacctgtcagggtcgtgtgttaagtcttaactggggcagaagatatagggaatctcttat	1740
QY	841	tggaaagtgaacagaggcctggagctgcagtggtctgtcgagctgtgtgtgtaaccttg	900	Db	1681	ataacctgtcagggtcgtgtgttaagtcttaactggggcagaagatatagggaatctcttat	1740

Qy 1741 taaactaacatgaatatgtgtcttcttccatttgcacaattcaataaagatacataatg 1800
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1741 taaactaacatgaatatgtgtcttcttccatttgcacaattcaataaagatacataatg 1800
 Qy 1801 ttctgtatgaaaaa 1813
 ||||||||||||||||
 Db 1801 ttctgtatgaaaaa 1813
 RESULT 2
 AAX28436
 ID AAX28436 standard; DNA; 1813 BP.
 XX
 AC AAX28436;
 XX
 DT 22-JUN-1999 (first entry)
 XX
 DE EGF-like homologue PRO246 coding sequence.
 XX
 KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261;
 PRO246;
 KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;
 KW FGF-8 homologue; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO914327-A2.
 XX
 PD 25-MAR-1999.
 XX
 PF 10-SEP-1998; 98WO-US18824.
 XX
 PR 25-NOV-1997; 97US-0066840.
 PR 17-SEP-1997; 97US-0059114.
 PR 17-SEP-1997; 97US-0059117.
 PR 18-SEP-1997; 97US-0059263.
 PR 15-OCT-1997; 97US-0062125.
 PR 17-OCT-1997; 97US-0062285.
 PR 17-OCT-1997; 97US-0062285.
 PR 24-OCT-1997; 97US-0062816.
 PR 29-OCT-1997; 97US-0063704.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA;
 PI Roy M, Wood WI;
 XX
 DR WPI; 1999-229532/19.
 DR P-PSDB; AAY05286.
 XX
 PT Antibodies against specific proteins overexpressed in tumours
 XX
 PS Example 1; Fig 27; 130pp; English.
 XX
 CC This sequence encodes the EGF-like homologue PRO246.
 CC The invention relates to antibodies (Ab) that bind to any of the
 CC polypeptides (I) designated PRO187; PRO533; PRO214; PRO240; PRO211;
 CC PRO230; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit

CC expression and/or activity of (I) are used: (i) to inhibit growth of
 CC tumours; and (ii) as diagnostic/prognostic reagents for detection or
 CC quantification of (I) in cells or tissues, by standard immunoassays,
 with
 CC overexpression being indicative of cancer. For therapeutic use, the Ab
 CC may be conjugated to a toxin, chemotherapeutic agent or radioisotope.
 CC Genes expressing (I), many of which are growth factor homologues, are
 CC overexpressed in some cases of cancer.

XX SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 20; Length 1813;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps
 0;

Qy 1 ggagccgcctgggtgtgcagcggctcggtcccgccagcgtccggccgtcgccagcct 60
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 Db 1 ggagccgcctgggtgtgcagcggctcggtcccgccagcgtccggccgtcgccagcct 60
 Qy 61 cggcacctgcaggtccgtgcgtcccgcggtggtggcccttgatccgtccggccagga 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 cggcacctgcaggtccgtgcgtcccgcggtggtggcccttgatccgtccggccagga 120
 Qy 121 gggtccatgatccctcccggggccccgtgtgacaaactgtcgcggtttgttcccg 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 gggtccatgatccctcccggggccccgtgtgacaaactgtcgcggtttgttcccg 180
 Qy 181 gggtgagtgccctcgccgccccctcgcgggcccgatgcacatgtgcccgaacc 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 gggtgagtgccctcgccgccccctcgcgggcccgatgcacatgtgcccgaacc 240
 Qy 241 gggtgcagggcggtggaagggaaggagtgtgtcttccagcgtgtacaccttgcagggg 300
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 Db 241 gggtgcagggcggtggaagggaaggagtgtgtcttccagcgtgtacaccttgcagggg 300
 Qy 301 aggtgtcttcatcccaaccatggagggtgccccttgtgagtgttcttcaacagaag 360
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 Db 301 aggtgtcttcatcccaaccatggagggtgccccttgtgagtgttcttcaacagaag 360
 Qy 361 aaaaggagatcagtggtgttctctacatcaatggggtcacacaagaacacctggagat 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 aaaaggagatcagtggtgttctctacatcaatggggtcacacaagaacacctggagat 420
 Qy 421 ccttgctactccatgccctcccggaacctgtccctgcggtggaagggtccaggaga 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 ccttgctactccatgccctcccggaacctgtccctgcggtggaagggtccaggaga 480
 Qy 481 aagactcggccctacagctgtccgtgaatgtgcaagacaagaaggcaatctagg 540
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 Qy 541 gccacagcatcaaaaccttagaactcaatgtactgttctccagctccatccctggcc 600
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Dh 601 gtctccagggtgtgtcccccatgtggtgggccaacgltgacccctgagctgcgcagctctccaagga 660
Qy 661 gtaagcccgctgtccaatataccaagtggatccggcagcttccatctctccaagacttctcttg 720
Dh 661 gtaagcccgctgtccaatataccaagtggatccggcagcttccatctctccaagacttctcttg 720
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Qy 781 ctggagctatgtctgtcgaaggcccaaatgagtggtgggacatgcctccaatgtaatgtgaagc 840
Dh 781 ctggagctatgtctgtcgaaggcccaaatgagtggtgggacatgcctccaatgtaatgtgaagc 840
Qy 841 tggaaagtgaagacagaggccttggaagctgcagtggttctgtgagagctgttgtggtaacctgg 900
Dh 841 tggaaagtgaagacagaggccttggaagctgcagtggttctgtgagagctgttgtggtaacctgg 900
Qy 901 ttggactggggttgcgtcgtggctgggtcctcttgcacacccgcgggggcaaggccttgg 960
Dh 901 ttggactggggttgcgtcgtggctgggtcctcttgcacacccgcgggggcaaggccttgg 960
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Dh 1021 agagctcagacaacaatctccaagaatgggaaccttctctctgtcacctccgcagagagccc 1080
Qy 1081 tccgggccaccccatggcctctcccaaggcctgtgtgcatgtgaccccccaagccagctctcca 1140
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Qy 1141 gccaggccctgcctctcaaccaagaactgcaccaagacagatggggcccaacctcaaccaatat 1200
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Dh 1201 ccccatcctcgtgtgggttctctcctcgtgcttgagcgcgcatgggtgtgtgcctgtga 1260
Qy 1261 tgggtgcctgcccagaatcaagctgtgctctcgtgatgatgaaccccaacctcaattggcta 1320
Dh 1261 tgggtgcctgcccagaatcaagctgtgctctcgtgatgatgaaccccaacctcaattggcta 1320
Qy 1321 aaggatttgggggtctctcctcctataaagggtcacacttaagcacagagggcctgagtcatg 1380
Dh 1321 aaggatttgggggtctctcctcctataaagggtcacacttaagcacagagggcctgagtcatg 1380
Qy 1381 ggaagaagtcacacatcctgaccccttagtactctgcccccaacctctcttactgtgggaaa 1440
Dh 1381 ggaagaagtcacacatcctgaccccttagtactctgcccccaacctctcttactgtgggaaa 1440
Qy 1441 accatctcagtaagaactaaagtgtccagagacagaagagagaagtggatctgga 1500
Dh 1441 accatctcagtaagaactaaagtgtccagagacagaagagagaagtggatctgga 1500

Qy 1501 attggagaggagctccaccccaacctgactcctctctatgaagccagctgtcgaatatg 1560
Dh 1501 attggagaggagctccaccccaacctgactcctctctatgaagccagctgtcgaatatg 1560
Qy 1561 ctactcaccaagagtgaaggggcagaagactccagtcactgaagctcccaagccccctga 1620
Dh 1561 ctactcaccaagagtgaaggggcagaagactccagtcactgaagctcccaagccccctga 1620
Qy 1621 tctgtaccccccaacctctatacaccaacctgtgctcccaactccagctccctgtatgat 1680
Dh 1621 tctgtaccccccaacctctatacaccaacctgtgctcccaactccagctccctgtatgat 1680
Qy 1681 ataacctgtcaggtcgtgctgttaagtttctaactggggcagaagataggaaatctctat 1740
Dh 1681 ataacctgtcaggtcgtgctgttaagtttctaactggggcagaagataggaaatctctat 1740
Qy 1741 taaactaacatgaatatgtgtgtttcatttcgaatttaataataagatacataatg 1800
Dh 1741 taaactaacatgaatatgtgtgtttcatttcgaatttaataataagatacataatg 1800
Qy 1801 ttgtatgaaaaa 1813
Dh 1801 ttgtatgaaaaa 1813

RESULT 3
AAA30052
ID AAA30052 standard; cDNA; 1813 BP.

XX AC AAA30052;
XX DT 09-AUG-2000 (first entry)
XX DE Human PRO246 nucleotide sequence.
XX KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261;
PRO246;
KW PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human;
KW cell growth; proliferation; cell surface virus receptor; ADPRT;
KW antibody dependent enzyme mediated prodnrg therapy; ss.
XX OS Homo sapiens.
XX PN WO200015666-A2.
XX PD 23-MAR-2000.
XX PF 08-SEP-1999; 99WO-US20594.
XX PR 10-SEP-1998; 98US-0099803.
XX PR 10-SEP-1998; 98WO-US18824.
XX PA (GETH) GEMENTECH INC.
XX PI Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI, Botstein D;
XX WPI; 2000-271386/23.
XX DR P-PSDB; AAY88574.

XX New isolated antibodies which bind to specific polypeptides used for
PT diagnosis and treatment of neoplastic cell growth and proliferation -
XX
PS Example 8; Fig 15; 200pp; English.
XX
CC This sequence represents a human PRO246 nucleotide sequence. PRO246 is
CC probably a cell surface virus receptor. The invention relates to
CC isolated
CC antibodies which bind to a polypeptide. The "PRO" polypeptides are
CC encoded by genes which are over expressed in the genome of tumour cells.
CC Vectors and host cells comprising the nucleic acid encoding the
CC antibodies are used in the production of the antibodies. The antibodies
CC and nucleic acids encoding them are used for diagnosing a tumour in a
CC mammal. The antibodies are used for inhibiting the growth of tumour
CC cells
CC and identifying compounds that inhibit a biological or immunological
CC activity of and/or expression of a PRO187, PRO533, PRO214, PRO240,
CC PRO211, PRO230, PRO261, PRO246 or PRO317 polypeptide. The antibody can
CC be
CC used in antibody dependent enzyme mediated prodrug therapy (ADEPT) by
CC conjugating the antibody to a prodrug-activating enzyme which converts
a
CC prodrug to an anti-cancer drug. The antibodies can be fluorescently
CC labelled and monitored by light microscopy, flow cytometry or
fluorimetry
CC for diagnosis and prognosis of tumours.
XX
SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 21; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggagccgcccgtgggtgtcagcggctcggctcccgccagctccggcgcagcct 60
Db 1 ggagccgcccgtgggtgtcagcggctcggctcccgccagctccggcgcagcct 60

QY 61 cggcacctgcaggtccgtgcgtcccgcgctggcgccctgaactccgtcccgccaggga 120
Db 61 cggcacctgcaggtccgtgcgtcccgcgctggcgccctgaactccgtcccgccaggga 120

QY 121 gggccatgattccctccgggggccccctgtgtgaccaactgtgcggttttgttctgg 180
Db 121 gggccatgattccctccgggggccccctgtgtgaccaactgtgcggttttgttctgg 180

QY 181 ggtcgaatgcccctcgccgccccctcgcgggcccaagtgtgacctgtgcccggcaacc 240
Db 181 ggtcgaatgcccctcgccgccccctcgcgggcccaagtgtgacctgtgcccggcaacc 240

QY 241 ggttcagagcgggtggaagggaagggaagtgtgtcttcagcgtgtgtacacctgtgacgggg 300
Db 241 ggttcagagcgggtggaagggaagggaagtgtgtcttcagcgtgtgtacacctgtgacgggg 300

QY 301 aggtgtcttcacccagccatgggaagggtgccccttgatgtgtgtcttcaacagagaag 360
Db 301 aggtgtcttcacccagccatgggaagggtgccccttgatgtgtgtcttcaacagagaag 360

Db 301 aggtgtcttcacccagccatgggaagggtgccccttgatgtgtgtcttcaacagagaag 360
QY 361 aaagaggatcaggtgtgtctctacatcaatggggtcacaaagaacactggaat 420
Db 361 aaagaggatcaggtgtgtctctacatcaatggggtcacaaagaacactggaat 420

QY 421 cctgtgtactccatgcccctccgggaacctgtccctgcgctggaagggttccaggaga 480
Db 421 cctgtgtactccatgcccctccgggaacctgtccctgcgctggaagggttccaggaga 480

QY 481 aagacttggccccctacagctgtccgtgaatgtgcaagacaacaaggcaatctagg 540
Db 481 aagacttggccccctacagctgtccgtgaatgtgcaagacaacaaggcaatctagg 540

QY 541 gccacagcatcaaaacctagactcaatgtactgtgtcttcacagctccatccctgccc 600
Db 541 gccacagcatcaaaacctagactcaatgtactgtgtcttcacagctccatccctgccc 600

QY 601 gtctccagggtgtgcccccatgtgggggcaaacgtgacctgagctgcccagctccaa 660
Db 601 gtctccagggtgtgcccccatgtgggggcaaacgtgacctgagctgcccagctccaa 660

QY 661 gtaagcccgctgtccaataccagtgagtcggcagcttccatccctccagacttcttg 720
Db 661 gtaagcccgctgtccaataccagtgagtcggcagcttccatccctccagacttcttg 720

QY 721 caccagcatatgattgtcatccgtgggtctttaaagcctcaccaacttctgtctccatg 780
Db 721 caccagcatatgattgtcatccgtgggtctttaaagcctcaccaacttctgtctccatg 780

QY 781 ctggagtcatagtctgcaaggcccaatgagtgggcactgcccgaatgtaatgtgacgc 840
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QY 841 tggaaatgagcacagggcctgtgagctcagtggtgtgtgtgagctgtgtggttaccc 900
Db 841 tggaaatgagcacagggcctgtgagctcagtggtgtgtgtgagctgtgtggttaccc 900

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Db 1021 agagctcagacaacaatctccaagaatggaaccttctctctgtacactccgacgagcc 1080

QY 1081 tccggcaccatggccctccagagctgtgtgcatgaccccaagccagctctctca 1140
Db 1081 tccggcaccatggccctccagagctgtgtgcatgaccccaagccagctctctca 1140

QY 1141 gccaggccctgcctcaccagactgcccacagacagatggggccacacctcaacaaat 1200
Db 1141 gccaggccctgcctcaccagactgcccacagacagatggggccacacctcaacaaat 1200

QY 1201 ccccatcctcgtggttcttctcctcgtcgtcgaagccgcatgggtgctgctgtga 1260
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 Db 1201 ccccatcctcgtggttcttctcctcgtcgtcgaagccgcatgggtgctgctgtga 1260
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 Db 1261 tgggtcctgcccagaagtcaagctggtcctcgtgatgatgaccccaatcatcgtgcta 1320
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 Db 1321 aaggaattgggggtcctcctcctccttaagggtaacactctagcacagaaggcctgaatcatg 1380
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 |||
 Db 1381 ggaagaagtcacacactcctgacccttagtactcctgccccacactccttactgtgggaaa 1440
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 QY 1441 accatctcagtaagaactaagtgtccagagacagagaagaagaagaagtgtgactgtga 1500
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 Db 1441 accatctcagtaagaactaagtgtccagagacagagaagaagaagaagtgtgactgtga 1500
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 QY 1501 atgggagagagcctccaccaccctgactcctccttatgaagcagctgctgaattag 1560
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 Db 1501 atgggagagagcctccaccaccctgactcctccttatgaagcagctgctgaattag 1560
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 Db 1561 ctactcaccaagaagtgaaggagagagactccactcactgactcctccagagcccttga 1620
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 Db 1621 tctgtacccccaccctatcctaaccaccacttgctccactccagctccctgtattgat 1680
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 Db 1681 ataacctgtcaggtcgtgtggttactggtgggagagagatagggaatccttat 1740
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 |||
 Db 1741 taaaactaacaatgaatatgtgtgttccatttccaatttaataaagatacataatg 1800
 |||
 QY 1801 ttgtatgaaaaa 1813
 |||
 Db 1801 ttgtatgaaaaa 1813
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RESULT 4
 AAS21412

ID AAS21412 standard; cDNA; 1813 BP.

XX AC AAS21412;

XX DT 24-OCT-2001 (first entry)

XX DE Human cDNA sequence encoding for PRO246 polypeptide.

KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal

muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000WO-US32678.
 XX
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI, 2001-408281/43.
 DR P-PSDB; AUI12340.
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical -
 XX
 PS Claim 3; Fig 337; 813pp; English.
 XX
 CC AAS21244-AAS21518 encode for novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing

Query Match	100.0%;	Score 1813;	DB 22;	Length 1813;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1813; Conservative	0;	Mismatches	0;	Indels 0; Gaps

0.

A vertical ruler with markings from 0 to 10 centimeters. The markings are in millimeters, with numbers every centimeter. The ruler is placed vertically on the right side of the page.

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661 gtaagcccgctgtccaataccagtcgggatcgcagcttcacatccttcagacttcttg 720

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Db 781 ctqqaqtctatgtctqcaaaqccccacaatqaaqtqqcactqcccaatqtaatqtqacc 840

QY 841 tggaaagtgaagcacaagggcctggagctgcagttgtctggagctgtgtgggtaccctgg 900

1. The first part of the document is a list of the names of the members of the committee, followed by a list of the names of the members of the sub-committee.

[illegible]

Db 961 agggagccagccaatgatatacaaggagatgcatgtccccggaacctgacctggccca 1020

1021 agagcttcagacatactcccaagaatcgggaccccttcctctgacaccctccgcagagccc 1080

[illegible]

Ov 114] accaaaccctaacccctacccaacaatvaccccaccaaaccctcaaaccaatat 1200

Db 1141 gccagggcctgccctcaccaagactggccacgacagatggggccaccctcaacaatat 1200

[illegible]

QY 1321 aaqgatttqqgtctctccttccctataaqqgtcacctctaqaacaaqaqqcctqaqtcatq 1380

Db 1321 aaggatttgsggtctctctctctctataagggtcaacctctagacagaggcctgattcatg 1380
Qy 1381 ggaagaagtcacactccttgacctagctactctgccccacctctcttactgtgggaa 1440
Db 1381 ggaagaagtcacactccttgacctagctactctgccccacctctcttactgtgggaa 1440
Qy 1441 accatctcagtaagaactaagtgtccaggagacagaaggagaaggaagtggatctgga 1500
Db 1441 accatctcagtaagaactaagtgtccaggagacagaaggagaaggaagtggatctgga 1500
Qy 1501 attggagagagctccaccacccttgactcctcttatgaagccagtgtgaattag 1560
Db 1501 attggagagagctccaccacccttgactcctcttatgaagccagtgtgaattag 1560
Qy 1561 ctactcaccagaagtgaggggcagagactccagtcactgagtctccagcccttga 1620
Db 1561 ctactcaccagaagtgaggggcagagactccagtcactgagtctccagcccttga 1620
Qy 1621 tctgtacccccaccctatctaacaccacccttgctcccaactccagctccctgtattgat 1680
Db 1621 tctgtacccccaccctatctaacaccacccttgctcccaactccagctccctgtattgat 1680
Qy 1681 ataactgtcaggctcgcttgtagtttactggggcagagatagggaatccttat 1740
Db 1681 ataactgtcaggctcgcttgtagtttactggggcagagatagggaatccttat 1740
Qy 1741 taaactaacatgaatatgtgtgttccatttgcgaatctaataaagatacataatg 1800
Db 1741 taaactaacatgaatatgtgtgttccatttgcgaatctaataaagatacataatg 1800
Qy 1801 ttctgatgaaaaa 1813
Db 1801 ttctgatgaaaaa 1813

RESULT 5

AAF60372

ID AAF60372 standard; cDNA; 1813 BP.

XX AAF60372;

AC AAF60372; (first entry)

DT 27-APR-2001

XX PRO246 coding sequence.

DE CYTOSTATIC; PRO protein; tumour; cancer; ss.

XX CYTOSTATIC; PRO protein; tumour; cancer; ss.

KW CYTOSTATIC; PRO protein; tumour; cancer; ss.

XX CYTOSTATIC; PRO protein; tumour; cancer; ss.

OS Homo sapiens.

XX Homo sapiens.

PN WO200105836-A1.

PD 25-JAN-2001.

XX 20-DEC-1999; 99WO-US30999.

PF 20-DEC-1999; 99WO-US30999.

XX 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28564.
XX (GETH) GENENTECH INC.
PA Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI;
XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI;
PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI;
XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI;
DR WPI; 2001-091968/10.
DR P-PSDB; AAB68599.
XX New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,
PT useful for diagnosing and treating cancers -
PS Claim 50; Fig 15; 196pp; English.
XX The present invention relates to PRO proteins and coding sequences. The
CC present sequence is the coding sequence for one such PRO protein.
CC It was found that the PRO genes are amplified in the genome of tumour
CC cells. The gene amplification is expected to be associated with the
CC overexpression of the gene product and contributes to tumourigenesis.
CC Therefore, antagonists of PRO proteins are useful for the treatment of
CC benign or malignant tumours, leukaemia, lymphoid malignancies and other
CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
CC epithelial, inflammatory and immunologic disorders.
XX Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;
SQ

Query Match 100.0%; Score 1813; DB 22; Length 1813;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps

0;

Qy 1 ggaagccgctgggtgtcagcggctcggtcccgcgacgctccgscgtcgcgagcct 60

Db 1 ggaagccgctgggtgtcagcggctcggtcccgcgacgctccgscgtcgcgagcct 60

Qy 61 cggcactgcaggtcgtgcgtcccgcgctggcgccccctgactccgtccggccaaggga 120

Db 61 cggcactgcaggtcgtgcgtcccgcgctggcgccccctgactccgtccggccaaggga 120

Qy 121 gggccatgatccctcccggggccccctggtgaaccaactgtcggttttgcctcgg 180

Db 121 gggccatgatccctcccggggccccctggtgaaccaactgtcggttttgcctcgg 180

Qy 181 ggtgagtgccctcgccccctcgcgggcccgacgtgaactgacattgcccccaacc 240

Db 181 ggtgagtgccctcgccccctcgcgggcccgacgtgaactgacattgcccccaacc 240

Qy 241 ggttcagcggtggaagggaagggaagtgtgtctccagcgtgtacacctgcagggg 300

Db 241 ggttcagcggtggaagggaagggaagtgtgtctccagcgtgtacacctgcagggg 300

Qy 301 aggtgtctcatcccgacgatggagggtgcctcttgatgtgttcttcaaacagaag 360

Db 301 aggtgtcttcatcccgacgatgagggtgccccttctgtgatgtgtctcttcaacagaaag 360
 Qy 361 aaaaggagatcagtggtgtgtcctacatcaatgagggtcacacaagaacactgagtat 420
 Db 361 aaaaggagatcagtggtgtgtcctacatcaatgagggtcacacaagaacactgagtat 420
 Qy 421 ccttggttactccatgctccctccggaaacctgtccctgcggtggaagggtctccaggaga 480
 Db 421 ccttggttactccatgctccctccggaaacctgtccctgcggtggaagggtctccaggaga 480
 Qy 481 aagactctggccctcagactgctccgtgaatgtgcaagacaacaaggcaaatctaggg 540
 Db 481 aagactctggccctcagactgctccgtgaatgtgcaagacaacaaggcaaatctaggg 540
 Qy 541 gccacagcatcaaaaaccttaagaactcaatgtactggtctctccagctcctccatcctgcc 600
 Db 541 gccacagcatcaaaaaccttaagaactcaatgtactggtctctccagctcctccatcctgcc 600
 Qy 601 gtctccagggtgtgcccccatgtgagggcaaacgtgaacctgagctgcagatctccaagga 660
 Db 601 gtctccagggtgtgcccccatgtgagggcaaacgtgaacctgagctgcagatctccaagga 660
 Qy 661 gtaagcccgctgtccaataaccagtggggtcggcagcttccatccttccagaacttctcttg 720
 Db 661 gtaagcccgctgtccaataaccagtggggtcggcagcttccatccttccagaacttctcttg 720
 Qy 721 caccagcatatagatgtcatccgtgggtctttaaagcctcaccaaccttctgtcttccatgg 780
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 Qy 781 ctggagctctatgtctcgaagcccaaatgaggtgggcactgcccgaatgtatgtgagcg 840
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 Qy 841 tggaaagtgaacacaaggccctggagctgcagtgtgtctgtagagctgttctgggtaccctgg 900
 Db 841 tggaaagtgaacacaaggccctggagctgcagtgtgtctgtagagctgttctgggtaccctgg 900
 Qy 901 ttggaactggggtgtgctggtcgtgggtcgtctcttctgaaccacgcggggcaaggccctgg 960
 Db 901 ttggaactggggtgtgctggtcgtgggtcgtctcttctgaaccacgcggggcaaggccctgg 960
 Qy 961 aggaagcagccaatgatatacaaggaggtgcatgtctcccgagacctgcccctggccca 1020
 Db 961 aggaagcagccaatgatatacaaggaggtgcatgtctcccgagacctgcccctggccca 1020
 Qy 1021 agagctcagacacaatctccaagaatgggacccttctctgtcacctccgcagagagccc 1080
 Db 1021 agagctcagacacaatctccaagaatgggacccttctctgtcacctccgcagagagccc 1080
 Qy 1081 tccggcaccatggccctcccgagcctgtgcatatgaaccgccagccagctctctcca 1140
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 Db 1141 gccaggccctgcccctcaccaagaactgcacgacagatggggcccaacctcaacaatat 1200

Qy 1201 ccccatcccttgggtgggttcttctcctctgcttgagccgcatgggtgtgtgtga 1260
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 Qy 1261 tggctgtgccagagtcaagctggtctctctgtatgatgacccaccatcattggtcta 1320
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 Qy 1321 aagatttgggtctctctcctctataagggtcacctctagcacagagccctgagtcagt 1380
 Db 1321 aagatttgggtctctctcctctataagggtcacctctagcacagagccctgagtcagt 1380
 Qy 1381 ggaagaagtacacatcctgacctagtaactctgccccacctctcttactgtgggaaa 1440
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 Qy 1441 accatctcagtaagacctaaagtgtccaggagacagaaggaggaagtgtgattcgtga 1500
 Db 1441 accatctcagtaagacctaaagtgtccaggagacagaaggaggaagtgtgattcgtga 1500
 Qy 1501 attggagaggagctccaccaccctgactcctcttatgaaagcagctgtgtaaatag 1560
 Db 1501 attggagaggagctccaccaccctgactcctcttatgaaagcagctgtgtaaatag 1560
 Qy 1561 ctactcaccaagatgagggggcagagactccagtcactgagctcccaagccctctga 1620
 Db 1561 ctactcaccaagatgagggggcagagactccagtcactgagctcccaagccctctga 1620
 Qy 1621 tctgtaccccaacctctatacaccaacctgtgctcccaacctcagctccctgtatgat 1680
 Db 1621 tctgtaccccaacctctatacaccaacctgtgctcccaacctcagctccctgtatgat 1680
 Qy 1681 ataactgtcaggctgtggtttaggttctaactggggcagagataggaaatctcttat 1740
 Db 1681 ataactgtcaggctgtggtttaggttctaactggggcagagataggaaatctcttat 1740
 Qy 1741 taaactaacatgaatatgtgtgtttcatattgcaaatctaaataaagatacataatg 1800
 Db 1741 taaactaacatgaatatgtgtgtttcatattgcaaatctaaataaagatacataatg 1800
 Qy 1801 ttgtatgaaaaa 1813
 Db 1801 ttgtatgaaaaa 1813

RESULT 6
 AAC87040
 ID AAC87040 standard; cDNA; 1813 BP.
 XX
 AC AAC87040;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Nucleotide sequence of human polypeptide PRO246.
 XX
 KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
 KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361;
 PRO1308;

KW PRO183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
 KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
 KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
 KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
 KW ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 126..1298
 FT sig_peptide 126..212
 FT /*tag= a
 FT /*tag= b
 XX
 XX WO200077037-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 22-MAY-2000; 2000WO-US14042.
 XX
 PR 15-JUN-1999; 99US-0139695.
 PR 20-JUL-1999; 99US-0145070.
 PR 26-JUL-1999; 99US-0145698.
 PR 17-AUG-1999; 99US-0149396.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28565.
 PR 07-DEC-1999; 99US-0169495.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 15-MAY-2000; 2000WO-US13358.
 PR 17-MAY-2000; 2000WO-US13705.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerlitsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX
 DR WPI; 2001-050091/06.
 DR P-PSDB; AAC87040.
 XX
 PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
 PT transmembrane polypeptide is useful for gene therapy and identification
 PT of related polypeptides -
 XX

PS Claim 2; Fig 57; 244pp; English.
 XX
 CC The present sequence encodes a human secreted and transmembrane
 CC polypeptide. The specification describes human polypeptides, designated
 CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
 CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
 CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
 CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
 CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
 CC can be modulated with agents that bind to these polypeptides, resulting
 CC in the death of the cells. The polynucleotides encoding these
 CC polypeptides are useful in the recombinant production of the
 CC polypeptides, as a hybridisation probe to screen libraries to isolate
 CC homologous sequences, or to map the gene. They may also be used for
 CC analysing genetic disorders, and to produce transgenic animals which are
 CC useful for the development and screening of therapeutically useful
 CC reagents. The polynucleotides can also be used in gene therapy e.g. to
 CC replace a defective gene.
 XX
 SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 22; Length 1813;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 ggaagccgcccgtgggtgtcagcgggtcggctcccgcgacgtccgscgtcgcgcaacct 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 ggaagccgcccgtgggtgtcagcgggtcggctcccgcgacgtccgscgtcgcgcaacct 60
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 QY 61 cggcacctgcaggtcgtgctgctcccgcggtcggcggcccttgatccgtccggccaagg 120
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 Db 61 cggcacctgcaggtcgtgctgctcccgcggtcggcggcccttgatccgtccggccaagg 120
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 QY 121 gggcgcattccctcccgggggccctgtgtaccacactgtcgcggtttgtcctcg 180
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 Db 121 gggcgcattccctcccgggggccctgtgtaccacactgtcgcggtttgtcctcg 180
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 QY 181 ggcgtgagtcctcgcgcggccctcgcgggcccagctgcaactgcatctgcccgaacc 240
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 Db 181 ggcgtgagtcctcgcgcggccctcgcgggcccagctgcaactgcatctgcccgaacc 240
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 QY 241 ggttcagcgcggtgagggagggaaagtgtgcttccagcgtgtgtacacctgtcacgggg 300
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 Db 241 ggttcagcgcggtgagggagggaaagtgtgcttccagcgtgtgtacacctgtcacgggg 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 aggtgtcttccatcccgacatggagaggtgaccttgtgtgtgttcttcaacagaag 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 aggtgtcttccatcccgacatggagaggtgaccttgtgtgtgttcttcaacagaag 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 361 aaaagagagatcaggtgtgttccctacatcaatgggggtcacacaagaacactggagtat 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 aaaagagagatcaggtgtgttccctacatcaatgggggtcacacaagaacactggagtat 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 421 cctgtgtactcatcagtcctcccggaacctgtccctgcggtgagaggtctccaggaga 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 cctgtgtactcatcagtcctcccggaacctgtccctgcggtgagaggtctccaggaga 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 481 aagacttggccctacagctgcctccgtgaatgttgcaagaacaacaggcaaatctaggg 540
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 Db 481 aagacttggccctacagctgcctccgtgaatgttgcaagaacaacaggcaaatctaggg 540
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 Qy 541 gccacagcatcaaaacctagaactcaatgtaactgttccctccagctcctccatccctggc 600
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 Db 541 gccacagcatcaaaacctagaactcaatgtaactgttccctccagctcctccatccctggc 600
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 Db 661 gtaagcccgctgtccaatacagctgggagtcggcagcttccatccttccaagacttctttg 720
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 Qy 721 caccagcattagatgtcatccgttgggtctttaagcctcaccaaccttgccttccatgg 780
 |||
 Db 721 caccagcattagatgtcatccgttgggtctttaagcctcaccaaccttgccttccatgg 780
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 Qy 781 ctgtagctatgtctgtcaaggcccaacaatgagtggtggcactgtcccaatgtatgtacgc 840
 |||
 Db 781 ctgtagctatgtctgtcaaggcccaacaatgagtggtggcactgtcccaatgtatgtacgc 840
 |||
 Qy 841 tggaaagtgaagcaaggccttgagctgcagctggttgcctgagagctgtgttgggtaccctgg 900
 |||
 Db 841 tggaaagtgaagcaaggccttgagctgcagctggttgcctgagagctgtgttgggtaccctgg 900
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 Qy 901 ttgtagtggtgtgtcgtgcttgggtcgtgctccttctgaaccacggccgggggcaaggccctgg 960
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 Db 901 ttgtagtggtgtgtcgtgcttgggtcgtgctccttctgaaccacggccgggggcaaggccctgg 960
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 Qy 961 aggaagccagccaatgatatacaaggagagatgcattgctcccggaacctgacctggccca 1020
 |||
 Db 961 aggaagccagccaatgatatacaaggagagatgcattgctcccggaacctgacctggccca 1020
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 Db 1021 agagctcagacaacaatctccaagaatgggagaccttctcctctgtcacctccgacagagccc 1080
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 Db 1081 tccggccaaccccatggcctcccaaggcctgtgtgcatlgaaccccaagcctcgtcttcca 1140
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 Qy 1141 gccaggccctgcctcaccagaactgcccacagacagatggggccaccctcaaccaatat 1200
 |||
 Db 1141 gccaggccctgcctcaccagaactgcccacagacagatggggccaccctcaaccaatat 1200
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 Qy 1201 ccccatcctctgttgggttcttctcctctgtgagcgcgcatgggtgtgtgcctgtga 1260
 |||
 Db 1201 ccccatcctctgttgggttcttctcctctgtgagcgcgcatgggtgtgtgcctgtga 1260
 |||
 Qy 1261 tggtagcttggcccaagatcaaagctggtctctgtgatgatgaaccccaactcatlgtgcta 1320
 |||
 Db 1261 tggtagcttggcccaagatcaaagctggtctctgtgatgatgaaccccaactcatlgtgcta 1320
 |||
 Qy 1321 aaggattgggggtctctcctctataagggtcacacttagcacagaggccttgatcatg 1380
 |||

Db 1321 aaggattgggggtctctcctctctataagggtcacacttagcacagaggccttgatcatg 1380
 |||
 Qy 1381 ggaagaagtcacactcctgaaccttgaactctgtcccccacactctcttaactgtgggaaa 1440
 |||
 Db 1381 ggaagaagtcacactcctgaaccttgaactctgtcccccacactctcttaactgtgggaaa 1440
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 Qy 1441 accatctcagtaagaacctaaagtgtccaggagacagaaggagaaggagtgatctgga 1500
 |||
 Db 1441 accatctcagtaagaacctaaagtgtccaggagacagaaggagaaggagtgatctgga 1500
 |||
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 |||
 Db 1501 attggaggagcctccaccacccctgaactcctccttatggaagccagctgtgaaatag 1560
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 Qy 1561 ctactcacaagaagtgaagggtcagaagactccagtcactgaactcctccaggcccttga 1620
 |||
 Db 1561 ctactcacaagaagtgaagggtcagaagactccagtcactgaactcctccaggcccttga 1620
 |||
 Qy 1621 tctgtaccccaacctatctaaccaccccttggctcccaactccagctccctgtatgat 1680
 |||
 Db 1621 tctgtaccccaacctatctaaccaccccttggctcccaactccagctccctgtatgat 1680
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 Qy 1681 ataactgtcaggtggtgttgaagtttctaactggggcagaagataggaaatctctat 1740
 |||
 Db 1681 ataactgtcaggtggtgttgaagtttctaactggggcagaagataggaaatctctat 1740
 |||
 Qy 1741 taaactaacatgaatatgtgtttcatttgcgaatttaaatgaatatcatatg 1800
 |||
 Db 1741 taaactaacatgaatatgtgtttcatttgcgaatttaaatgaatatcatatg 1800
 |||
 Qy 1801 ttgtatgaaaaa 1813
 |||
 Db 1801 ttgtatgaaaaa 1813
 |||

RESULT 7
 AAF72379
 ID AAF72379 standard; cDNA; 1813 BP.
 XX
 AC AAF72379;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human PRO246 cDNA.
 XX
 KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
 KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
 KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
 KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation; se.
 XX
 OS Homo sapiens.
 XX
 PN WO200104311-A1.
 XX
 PD 18-JAN-2001.
 XX

Pf 22-FEB-2000; 2000WO-US04414.
XX
PR 07-JUL-1999; 99US-0143048.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 99WO-US00219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI; 2001-081051/09.
DR P-PSDB; AAB80219.
XX
PT Sixty one nucleic acids encoding PRO polypeptides which are useful in
PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
PT Alzheimer's disease) -
PT Alzheimer's disease)
XX
XX Claim 2; Fig 16; 393pp; English.
XX
CC The present sequence is one of sixty one nucleic acids encoding novel
CC secreted and transmembrane PRO polypeptides. The PRO polypeptides are
CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
CC squamous cell carcinoma), gastrointestinal disorders (e.g.
CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
CC endometrial bleeding angiogenesis, ischaemias such as coronary
CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
CC diabetes and retinal disorders such as retinitis pigmentosum.
CC The PRO nucleic acids have applications in molecular biology, including
CC use as hybridization probes, and in chromosome and gene mapping.
XX
SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 22; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps

1 ggagccgacctgtgtgtcagcggtcgcgtcccgcgacagctccggcgtcgcagcct 60
|||||

Db 1 ggagccgacctgtgtgtcagcggtcgcgtcccgcgacagctccggcgtcgcagcct 60
Qy 61 cggcacctgcaggtccgtgcgtcccgcggtcggcgccctgaatccgtcccgccaggga 120
|||||
Db 61 cggcacctgcaggtccgtgcgtcccgcggtcggcgccctgaatccgtcccgccaggga 120
Qy 121 gggccatgatctccctcccggggccccctgtgtgaccaactgtgcggtttttgtctctg 180
|||||
Db 121 gggccatgatctccctcccggggccccctgtgtgaccaactgtgcggtttttgtctctg 180
Qy 181 ggtgagtgccctcgccccctcgcgggccagctgcaactgcaactgcccgcgaacc 240
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Db 181 ggtgagtgccctcgccccctcgcgggccagctgcaactgcaactgcccgcgaacc 240
Qy 241 ggttcaggcggtggaagggaagggtgtgctccagcgtgtacaccttgacgggg 300
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Db 241 ggttcaggcggtggaagggaagggtgtgctccagcgtgtacaccttgacgggg 300
Qy 301 agtgtcttcacatccagcatgggaaggtgcccttgtgatgtgtcttcaacagaag 360
|||||
Db 301 agtgtcttcacatccagcatgggaaggtgcccttgtgatgtgtcttcaacagaag 360
Qy 361 aaaaggagatcaggtgtgtcctacatcaatgggggtcacacaagaacaaacttgagtat 420
|||||
Db 361 aaaaggagatcaggtgtgtcctacatcaatgggggtcacacaagaacaaacttgagtat 420
Qy 421 cctgtgtactcactcagtcctcccggaacctgtccctcgcggtgaggggtctccaggaga 480
|||||
Db 421 cctgtgtactcactcagtcctcccggaacctgtccctcgcggtgaggggtctccaggaga 480
Qy 481 aagactctggccctacagctcgtcgtgaatgtgacaagacaagaagcaatctaggg 540
|||||
Db 481 aagactctggccctacagctcgtcgtgaatgtgacaagacaagaagcaatctaggg 540
Qy 541 gccacagcatcaaaaccttagaactcaatgtactgttccctccagctccatccctcgc 600
|||||
Db 541 gccacagcatcaaaaccttagaactcaatgtactgttccctccagctccatccctcgc 600
Qy 601 gtctccagggtgtgcccccatgtgggggcaaaagtgaacctgagctgcccagttccaagga 660
|||||
Db 601 gtctccagggtgtgcccccatgtgggggcaaaagtgaacctgagctgcccagttccaagga 660
Qy 661 gtaagccgctgtccaatacagtgtagtcggcagcttccatccctccagacttctctg 720
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Db 661 gtaagccgctgtccaatacagtgtagtcggcagcttccatccctccagacttctctg 720
Qy 721 caccagcatgatgtcatccgtgggtctttaagcctcaccaaccttgcttccatgg 780
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Db 721 caccagcatgatgtcatccgtgggtctttaagcctcaccaaccttgcttccatgg 780
Qy 781 ctggaagtcatgtctgcaagggccacaatgaggtgggcactgcccgaatgtaagtgaagc 840
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Db 781 ctggaagtcatgtctgcaagggccacaatgaggtgggcactgcccgaatgtaagtgaagc 840
Qy 841 tggaaagtgaagcaggggctgagctgcagctggtgtgtggaagtgtgtgggtacacctgg 900
|||||
Db 841 tggaaagtgaagcaggggctgagctgcagctggtgtgtggaagtgtgtgggtacacctgg 900

XX New isolated nucleic acid for producing a PRO polypeptide, analyzing
PT genetic disorders and treating cardiovascular, endothelial or
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -
XX
PS Claim 58; Fig 37; 293pp; English.
XX
CC The invention relates to novel human angiogenesis-associated proteins
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
CC PRO proteins. The invention also relates to vectors and host cells
CC comprising a PRO nucleic acid, the recombinant production of a PRO
CC protein, PRO antibodies specific for a PRO protein, fusion proteins
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
CC compounds which inhibit the expression of a PRO gene. The invention
CC additionally encompasses methods of identifying modulators of PRO
CC expression or activity; diagnosing a cardiovascular, endothelial or
CC angiogenic disorder, or a susceptibility to such a disorder by detecting
CC mutations in a PRO gene, or the expression level of a PRO gene within a
CC particular tissue; treating a cardiovascular, endothelial or angiogenic
CC disorder via the administration of a PRO protein, PRO nucleic acid, or
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising
a
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
CC administration of a PRO protein, or an agonist or antagonist thereof.
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
CC agonists and PRO antagonists may be used as therapeutic agents to treat
CC cardiovascular, endothelial or angiogenic disorders, such as
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
CC disease, or stroke. PRO nucleic acids are additionally useful in the
CC recombinant production of PRO proteins, as hybridisation probes to
CC screen libraries to isolate cDNAs with sequence identity to PRO
CC proteins,
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
CC gene therapy. PRO nucleic acids can also be used to produce transgenic
CC animals useful for the development and screening of potential
CC therapeutic agents. The present sequence represents a cDNA encoding a
PRO
CC protein of the invention.
XX
SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;
XX
Query Match 100.0%; Score 1813; DB 22; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

QY 121 gggccatgattccctcccggggcccctgtgaccaaactgtgcggttttctgctcgg 180
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Db 121 gggccatgattccctcccggggcccctgtgaccaaactgtgcggttttctgctcgg 180
QY 181 ggtgagtgccctcgcgcccccctcgcgggccagctgcgaactgcacttgcgcgaacc 240
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Db 181 ggtgagtgccctcgcgcccccctcgcgggccagctgcgaactgcacttgcgcgaacc 240
QY 241 ggttcgagcggttgagaggagggaggtgtgtctccagcgtgtgtacacttgcagcggg 300
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Db 241 ggttcgagcggttgagaggagggaggtgtgtctccagcgtgtgtacacttgcagcggg 300
QY 301 aggtgtcttcaccccgacatggagagtgcccttgtgatgtgttcttcaacagaaag 360
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Db 301 aggtgtcttcaccccgacatggagagtgcccttgtgatgtgttcttcaacagaaag 360
QY 361 aaagagagatcagtggtgttcctacatcatatggggtcacacaagaacacttgagtat 420
|||
Db 361 aaagagagatcagtggtgttcctacatcatatggggtcacacaagaacacttgagtat 420
QY 421 cctgtgtactcatcgtccctccggaaacctgtccctgcggttgagaggtctccagaga 480
|||
Db 421 cctgtgtactcatcgtccctccggaaacctgtccctgcggttgagaggtctccagaga 480
QY 481 aagacttggccctacagctgcctcggtgaatgtgcagaacaagaagcaatctcaggg 540
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Db 481 aagacttggccctacagctgcctcggtgaatgtgcagaacaagaagcaatctcaggg 540
QY 541 gccacagcatcaaaaccttagaactcaatgttcttccagctccctccatcccgcc 600
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Db 541 gccacagcatcaaaaccttagaactcaatgttcttccagctccctccatcccgcc 600
QY 601 gtctccagagtggtgcccctatgtgggggcaaacgtgacccctgagctgcagctcccaagg 660
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Db 601 gtctccagagtggtgcccctatgtgggggcaaacgtgacccctgagctgcagctcccaagg 660
QY 661 gtaagccgctgtccaataccagtggtgatcggcagcttccatccttccagactttcttg 720
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Db 661 gtaagccgctgtccaataccagtggtgatcggcagcttccatccttccagactttcttg 720
QY 721 caccagcatatgattcatccgtggtgtcttaagcctcaaccaacttctgtcttccatgg 780
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Db 721 caccagcatatgattcatccgtggtgtcttaagcctcaaccaacttctgtcttccatgg 780
QY 781 ctggagtctatgtctgcaaggccacatgaggtgggacatgcccaatgttaatgtgacgc 840
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Db 781 ctggagtctatgtctgcaaggccacatgaggtgggacatgcccaatgttaatgtgacgc 840
QY 841 ttgaagtgaagcaagggctctgagctgagtggtgtctgagactgtgtgtgtacacctgg 900
|||
Db 841 ttgaagtgaagcaagggctctgagctgagtggtgtctgagactgtgtgtgtgtacacctgg 900
QY 901 ttggaactggggtgtgtgctggctggtgtcctcttgtaaccacgcgaggggcagggccttgg 960
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Db 901 ttggaactggggtgtgtgctggctggtgtcctcttgtaaccacgcgaggggcagggccttgg 960
QY 961 aggagccagccaatgatatacaaggagatgtccattgtcccggaacctgtgcctgtgcaca 1020
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Db 961 aggagccagccaatgatatacaaggagatgccattgtctcccggaacctgtgcccctgtgccc 1020

QY 1021 agagctcagacacaatctccaagaatggagacctctctctgtcacctccgcagagacc 1080

Db 1021 agagctcagacacaatctccaagaatggagacctctctctgtcacctccgcagagacc 1080

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Db 1201 ccccatccctggtggggttctctctctgtgctgagccgcatgggtgtgtgtgtga 1260

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Db 1261 tgggtgctgccccagagtcaagctgtgctctctgtatgatgacccaccatcttggtcta 1320

QY 1321 aaggaattgggggtctctctctctataagggtcacctctagcacagagggctgtgcatg 1380

Db 1321 aaggaattgggggtctctctctctataagggtcacctctagcacagagggctgtgcatg 1380

QY 1381 ggaagagtcacactctgacctagtactctgccccacctctcttactgtgggaaa 1440

Db 1381 ggaagagtcacactctgacctagtactctgccccacctctcttactgtgggaaa 1440

QY 1441 accatctcagtaagacctaaagtgtccagagacagaagagaagagaagtgtgactgtga 1500

Db 1441 accatctcagtaagacctaaagtgtccagagacagaagagaagagaagtgtgactgtga 1500

QY 1501 attggagagagctccaccaccctgactcctccttatgaagccagctgtctgaatatag 1560

Db 1501 attggagagagctccaccaccctgactcctccttatgaagccagctgtctgaatatag 1560

QY 1561 ctactccaccaagagtggaggggcagagactccagtcactgagctcccaagggcccttga 1620

Db 1561 ctactccaccaagagtggaggggcagagactccagtcactgagctcccaagggcccttga 1620

QY 1621 tctgtacccccaccctatctaaccaccctgtgtcccaactccagctccctgtatgat 1680

Db 1621 tctgtacccccaccctatctaaccaccctgtgtcccaactccagctccctgtatgat 1680

QY 1681 ataacctgtcaggtcgtgtgttaggtttactctggggcagagatagggaatctcttat 1740

Db 1681 ataacctgtcaggtcgtgtgttaggtttactctggggcagagatagggaatctcttat 1740

QY 1741 taaaactaacaatgaatatgtgtgtttcatcttgaatttaaatgaagatacataatg 1800

Db 1741 taaaactaacaatgaatatgtgtgtttcatcttgaatttaaatgaagatacataatg 1800

QY 1801 ttctgtatgaaaaa 1813

Db 1801 ttctgtatgaaaaa 1813

RESULT 9
AAFP93785

ID AAFP93785 standard; cDNA; 1821 BP.

XX

AC AAFP93785;

XX

DT 23-MAY-2001 (first entry)

XX

DE Human cDNA encoding a membrane or secretory protein clone PSEC0086.

XX

KW Human; secretory protein; membrane protein; vaccine; gene therapy;

KW rheumatoid arthritis; diabetes; ss.

XX

OS Homo sapiens.

XX

PN EP1067182-A2.

XX

PD 10-JAN-2001.

XX

PF 07-JUL-2000; 2000EP-0114090.

XX

PR 08-JUL-1999; 99JP-0194179.

PR 11-JAN-2000; 2000JP-0118775.

PR 02-MAY-2000; 2000JP-0183766.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

XX

DR WPI; 2001-093989/11.

DR P-PSDB; AAB88358.

XX

PT Nucleic acids encoding secretory proteins/membrane proteins, useful in

PT gene therapy or as candidate target molecules in drug development -

XX

PS Claim 1; SEQ ID 83; 609pp + CD ROM; English.

XX

CC This invention relates to nucleic acid sequences AAFP93744 - AAFP93916

CC which encode human secretory or membrane proteins represented by

CC AAB88317 - AAB88419. Included in the invention are primers

CC AAFP93917 - AAFP94295 and AAFP62232 - AAFP62235 which are used to isolate

the

CC cDNA sequences of the invention. The invention also includes methods for

CC the production of antibodies directed against the proteins, and cDNA

CC sequences, which can be used in vaccines. The polynucleotide sequences

CC can be used in gene therapy. The polynucleotide sequences and the

CC proteins they encode may be used in the prevention, treatment and

CC diagnosis of diseases associated with inappropriate secretory

CC protein/membrane protein expression. The nucleic acids and complementary

CC sequences may also be used as DNA probes in diagnostic assays

CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the

CC presence of similar nucleic acid sequences in samples. They may also be

CC used to study the expression and function of secretory proteins/membrane

CC polypeptides and their role in metabolism. The polypeptides may be used

CC as antigens in the production of antibodies against them and in assays

to

CC identify modulators (agonists and antagonists) of expression and

CC activity. The antibodies and antagonists may also be used as therapeutic

CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.

XX Sequence 1821 BP; 366 A; 561 C; 489 G; 405 T; 0 other;

Query Match 99.8%; Score 1809; DB 22; Length 1821;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggaagccgcctgggtgtcagcggtccgcgcgcagctccggcctgcgcagacct 60
DB 12 ggaagccgcctgggtgtcagcggtccgcgcgcagctccggcctgcgcagacct 71
QY 61 cggcacctgcaggtccggtgcgtccgcgcgcgtggcgcctgaactccgcccagagga 120
DB 72 cggcacctgcaggtccggtgcgtccgcgcgcgtggcgcctgaactccgcccagagga 131
QY 121 gggccatgatctccctccggggccctcgtgtgacccaactgtgcggttttctcctgg 180
DB 132 gggccatgatctccctccggggccctcgtgtgacccaactgtgcggttttctcctgg 191
QY 181 ggcgtggtgcctcgcgcgcctccgcgcgcgcagctgcaactgtcactgtccgcgcaacc 240
DB 192 ggcgtggtgcctcgcgcgcctccgcgcgcgcagctgcaactgtcactgtccgcgcaacc 251
QY 241 ggttcgagcggtggaaggagggaaagtgtgtctccagcgtggtacacctgtcacgagg 300
DB 252 ggttcgagcggtggaaggagggaaagtgtgtctccagcgtggtacacctgtcacgagg 311
QY 301 aggtgtctcatccacgacatgggaagtgcctctgtgatgtgtcttcaacagagaag 360
DB 312 aggtgtctcatccacgacatgggaagtgcctctgtgatgtgtcttcaacagagaag 371
QY 361 aaaaggaagatcagtggttctcctacatcaatggggtcacacaagaacaaactgagatat 420
DB 372 aaaaggaagatcagtggttctcctacatcaatggggtcacacaagaacaaactgagatat 431
QY 421 ccttggtctactccatgcctcccggaacgttcctcgtgcgtggaaggtctccagagaga 480
DB 432 ccttggtctactccatgcctcccggaacgttcctcgtgcgtggaaggtctccagagaga 491
QY 481 aagactctgccccctacagctgtccgtgaatgtgcagaagaacaaggaactcaggg 540
DB 492 aagactctgccccctacagctgtccgtgaatgtgcagaagaacaaggaactcaggg 551
QY 541 gccacagcatcaaaaccttagaactcaatgtaactgttcctccagctcctccatcctgcc 600
DB 552 gccacagcatcaaaaccttagaactcaatgtaactgttcctccagctcctccatcctgcc 611
QY 601 gtctccaggtgtgcccccatgtgggggcaaacgtgacccctgagctgccaactccaagga 660
DB 612 gtctccaggtgtgcccccatgtgggggcaaacgtgacccctgagctgccaactccaagga 671

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DB 672 gtaagcccgctctccaataccagtggtatcggcagcttccatcctccagactttcttg 731
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QY 781 ctggagttctatctctgcaaggcccaatgaagtgggcaactgccaatgtatgtgagcc 840
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QY 1141 gccagggcctgtgcctcacaaagactgcccacagacagatgggggccaacctcaaccaatat 1200
DB 1152 gccagggcctgtgcctcacaaagactgcccacagacagatgggggccaacctcaaccaatat 1211
QY 1201 cccccaatccctgtgtggggttcttctcctctgtgcttgagccgcatgggtgtgtgtgtga 1260
DB 1212 cccccaatccctgtgtggggttcttctcctctgtgcttgagccgcatgggtgtgtgtgtga 1271
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DB 1272 tgggt 1331
QY 1321 aaggattggggtctctccttccctataaggttcacctctagcacagagggcctgagtcatg 1380
DB 1332 aaggattggggtctctccttccctataaggttcacctctagcacagagggcctgagtcatg 1391
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DB 1392 ggaagaagtcacactcctgaaccttagtaactgtgcccccaacctctcttaactgtgggaaa 1451
QY 1441 accatctcagtaagaaccttaagtgctccaggagacagaaggagaaggaagtgtgactctgga 1500
DB 1452 accatctcagtaagaaccttaagtgctccaggagacagaaggagaaggaagtgtgactctgga 1511
QY 1501 attggggagagcttccaccacccctgactcctccttatgaagcagctgtcgaatatag 1560

Db 1512 attgaggagagctccaccacccttgactcctccttatgaagcagctgctgaattag 1571
Qy 1561 ctactaccagaagtgagggcagagactccagtcactgaagctccaggcccttga 1620
Db 1572 ctactaccagaagtgagggcagagactccagtcactgaagctccaggcccttga 1631
Qy 1621 tctgtaccaccaccctatctaacaccacccttgctcccaactccagctccctgtatgat 1680
Db 1632 tctgtaccaccaccctatctaacaccacccttgctcccaactccagctccctgtatgat 1691
Qy 1681 ataactgtcaggtcgtggttgaagtttactggggcagagatagggaattccttat 1740
Db 1692 ataactgtcaggtcgtggttgaagtttactggggcagagatagggaattccttat 1751
Qy 1741 taaactaacatgaatatgtgtgttccatttgcaatttaataagaatatacatatg 1800
Db 1752 taaactaacatgaatatgtgtgttccatttgcaatttaataagaatatacatatg 1811
Qy 1801 ttgtcatga 1809
Db 1812 ttgtcatga 1820

RESULT 10
AAH02949

ID AAH02949 standard; DNA; 1827 BP.
XX
AC AAH02949;
XX
DT 15-JUN-2001 (first entry)
XX
DE Human shear stress-response coding sequence SEQ ID NO: 143.
XX
KW Human; shear stress-response protein; vascular disease;
KW arteriosclerosis; ds.
XX
OS Homo sapiens.
XX
PN WO200125427-A1.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-JP06840.
XX
PR 01-OCT-1999; 99JP-0280976.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (NOJI/) NOJIMA H.
XX
PI Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
PI Kuga T, Sekine S, Nakamura Y, Sugano S;
XX
DR WPI; 2001-266308/27.
DR P-PSDB; AAB90818.
XX
PT DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis -

XX
PS Claim 1; Page 595-599; 678pp; Japanese.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PTCA restenosis and
CC hypertension.
XX
SQ Sequence 1827 BP; 369 A; 559 C; 491 G; 408 T; 0 other;

Query Match 99.6%; Score 1806.6; DB 22; Length 1827;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1809; Conservative 0; Mismatches 4; Indels 0; Gaps

Qy 1 ggaagccgcccgtgggtgtcagcggctcggctcccgcgacgctccggcgtcggcagcct 60
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Qy 61 cggcacctgcaggtccggtcgtcccgcggtcggcggcccttgactccgtcccgccagggga 120
Db 73 cggcacctgcaggtccggtcgtcccgcggtcggcggcccttgactccgtcccgccagggga 132
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Qy 421 cctgtgtactccatcgccctcccggaacctgtccctgcggtcgtgagggtctccagagaga 480
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Db 493 aagactctggccctacagctgtcctcgtgaatgtgcagaacaaacaggcaaatctaagg 552
Qy 541 gccacagcatcaaaaccttagaactcaatgtactgtgtctctccagctcctccatcctgccc 600
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 Qy 1741 taaactcaacatgaataatgtgtgtttcatttgcgaattcaataagaatacataatg 1800
 Db 1753 taaactcaacatgaataatgtgtgtttcatttgcgaattcaataagaatacataatg 1812
 Qy 1801 ttgtatgaaaaa 1813
 Db 1813 ttgtatgagata 1825
 RESULT 11
 AAD12605
 ID AAD12605 standard; cDNA; 1816 BP.
 XX AC AAD12605;
 XX DT 25-SEP-2001 (first entry)
 XX DE Human protein having hydrophobic domain encoding cDNA clone HP10801.
 KW Human; hydrophobic domain; gene therapy; nutritional supplement;
 KW cell proliferation; immunomodulatory; autoimmune disorder;
 KW antimicrobial;
 KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
 KW haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
 KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
 KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
 KW contraceptive; antiinfertility; antiinflammatory; ss.
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FH CDS 134..1306
 FT /*tag= a
 FT /product= "Human protein having hydrophobic domain"
 FT /note= "CDS is specifically is claimed in claim 3"
 FT sig_peptide 134..223
 FT /*tag= b
 FT mat_peptide 224..1303
 FT /*tag= c
 FT /product= "Mature human protein with hydrophobic domain"
 XX
 PN WO200149728-A2.

Db 849 tggaaagtgaagcacaaaggccttgagctgcagtcggttgctgtagagctgtgtggtgtacccttg 908
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Db 1749 taaactaacatgaatatgtgtgttctcatttgcaaatttaaatgaatacataatg 1808
Qy 1801 ttgtgatg 1808
Db 1809 ttgtgatg 1816

RESULT 12

AAA23441
ID AAA23441 standard; cDNA; 1954 BP.

AC AAA23441;

DT 19-JUN-2000 (first entry)

DE cDNA encoding human secreted protein vc51_1, SEQ ID NO:37.

KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW neurodegenerative disease; asthma; contraceptive; ss.

OS Homo sapiens.

FN Key Location/Qualifiers
FT CDS 139..1311
FT /tag= a
FT /product= "Human secreted protein vc51_1"

PN WO200011015-A1.

PD 02-MAR-2000.

PF 24-AUG-1999; 99WO-US19351.

XX 24-AUG-1998; 98US-0097638.

PR 24-AUG-1998; 98US-0097659.

PR 09-SEP-1998; 98US-0099618.

PR 28-SEP-1998; 98US-0102092.

PR 25-NOV-1998; 98US-0109978.

PR 23-DEC-1998; 98US-0113645.

PR 23-DEC-1998; 98US-0113646.

PR 23-AUG-1999; 99US-0379246.

XX (ALPH-) ALPHAGENE INC.

PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

DR WPI; 2000-224657/19.
DR P-PSDB; AAY94999.

PT New secreted or transmembrane proteins and polynucleotides encoding
PT them, useful for treating neurodegenerative disorders, autoimmune
PT diseases and cancer -
XX Claim 46; Page 296; 357pp; English.

:XX The invention relates to 40 human secreted proteins (AAV94981-Y95020),
 CC and cDNA sequences encoding them (AAA23423-A23462). The secreted
 CC proteins of the invention include those that are thought to be only
 CC partially secreted, i.e., transmembrane proteins. The proteins of the
 CC invention may exhibit one or more activities selected from the
 following:
 CC cytokine activity; cell proliferation; differentiation; immune
 CC modulation; haematopoiesis regulation; tissue growth activity;
 CC activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic
 CC and thrombolytic activity; anti-inflammatory activity; and tumour
 CC inhibition activity. The proteins may be administered to patients as
 CC vaccines, and the nucleotides may be used as part of a gene therapy
 CC regime. Diseases or conditions that may be treated using the proteins or
 CC nucleotides of the invention include autoimmune diseases; genetic
 CC disorders; haemophilia; cardiovascular diseases; cancer; bacterial,
 CC fungal and viral infections, especially HIV; multiple sclerosis;
 CC rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;
 CC insulin dependent diabetes mellitus; and allergic reactions such as
 CC asthma and anaemia. They may also be used for treating wounds, burns,
 CC ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease and amyotrophic
 CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may
 CC additionally be useful as contraceptives. Nucleic acid sequences of the
 CC invention may be used in chromosome mapping, and as a source of
 CC diagnostic primers and probes. The present sequence represents cDNA
 CC encoding one of the 40 proteins of the invention.
 XX
 SQ Sequence 1954 BP; 498 A; 561 C; 490 G; 405 T; 0 other;

Query Match 99.4%; Score 1802; DB 21; Length 1954;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1813; Conservative 0; Mismatches 0; Indels 1; Gaps

QY 1 ggagccgcccctgggtgtcagc-ggctcgcgtcccgccgacgctccggcctgcgcgacgc 59
 Db 13 ggagccgcccctgggtgtcagcgggtcgcgtcccgccgacgctccggcctgcgcgacgc 72
 QY 60 tcgcacactgcaggtccgtgcgtcccgcgagctgcgccttcgactccgtcccgccaggg 119
 Db 73 tcgcacactgcaggtccgtgcgtcccgcgagctgcgccttcgactccgtcccgccaggg 132
 QY 120 agggccatgatcttcctcccgggggccctggtgacccaactgctgcggttttgcctg 179
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 QY 180 gggctgagtgccctcgcgcccccctcgggccccagctgcaactgcaactgccccccaac 239
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Db 313 gaggtgtcttcattccacgcatgggaggtgccttctgtatgtgtgttcttcaacagaaa 372
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 Db 493 aaagactctggccctcactagctgtccgtgaatgtgcaagacaagcaaacctcagg 552
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 Db 733 gcaccagcatatgatgtatccgtggtgtcttaagcctcacaaccttgcgttccatg 792
 QY 780 gctgagctatagtctgcgaaggcccaaatgagtgggcactgcccagtatgtacg 839
 Db 793 gctgagctatagtctgcgaaggcccaaatgagtgggcactgcccagtatgtacg 852
 QY 840 ctggaagtgaagcacaggccctggagctgcagtggtgtgctggaagctgtgtgggtaccc 899
 Db 853 ctggaagtgaagcacaggccctggagctgcagtggtgtgctggaagctgtgtgggtaccc 912
 QY 900 gttgactggggtgtgctgcgtggcgtggtcctctgtacacccgcggggcgaagccctg 959
 Db 913 gttgactggggtgtgctgcgtggcgtggtcctctgtgtacacccgcggggcgaagccctg 972
 QY 960 gaggaagcagccaatgatatacaaggagatgccaatgtctcccggaacctgtgcctggccc 1019
 Db 973 gaggaagcagccaatgatatacaaggagatgccaatgtctcccggaacctgtgcctggccc 1032
 QY 1020 aagagctcagacacaactctccaagaatgggaccttctctctgtcactctcgacagagcc 1079
 Db 1033 aagagctcagacacaactctccaagaatgggaccttctctctgtcactctcgacagagcc 1092
 QY 1080 ctccggcaaccatgtgcctccacagcctgtgtgcatgtgacccccaagcagctctcc 1139
 Db 1093 ctccggcaaccatgtgcctccacagcctgtgtgcatgtgacccccaagcagctctcc 1152
 QY 1140 agccagggcctgcctcaccagaagctcccacagacagatggggccaccctcaaccata 1199
 Db 1153 agccagggcctgcctcaccagaagctcccacagacagatggggccaccctcaaccata 1212

QY 1200 tccccatccctggtggggttctctctgctggtctgaagccgcatgggtgctgtgctgtg 1259
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 Db 1213 tccccatccctggtggggttctctctgctggtctgaagccgcatgggtgctgtgctgtg 1272
 QY 1260 atggtgctgcccagagtcaagctggctctctggtatgatgacccaccatcatggct 1319
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 Db 1273 atggtgctgcccagagtcaagctggctctctggtatgatgacccaccatcatggct 1332
 QY 1320 aaaggtattgggggtctctctctctataagggtcaacctctagcacagaggctgagtcac 1379
 |||||
 Db 1333 aaaggtattgggggtctctctctctataagggtcaacctctagcacagaggctgagtcac 1392
 QY 1380 gggaaagagtcacacctctgacctagtcactctgccccaccctctcttactgtggaa 1439
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 Db 1393 gggaaagagtcacacctctgacctagtcactctgccccaccctctcttactgtggaa 1452
 QY 1440 aaccatctcagtaagaacctaaagtgtccagagacagagaaggaaggaagtgtgactctg 1499
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 Db 1453 aaccatctcagtaagaacctaaagtgtccagagacagagaaggaaggaagtgtgactctg 1512
 QY 1500 aattgggagggagcctccaccaccctgactcctccttatgaagccaagctgtgaaatla 1559
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 Db 1513 aattgggagggagcctccaccaccctgactcctccttatgaagccaagctgtgaaatla 1572
 QY 1560 gctactcaccaagagtgaggggagagagactccagtcactgagtcctccaggcccttg 1619
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 Db 1573 gctactcaccaagagtgaggggagagagactccagtcactgagtcctccaggcccttg 1632
 QY 1620 atctgtacccccaccctatcttaacaccacccttggtcctccactccagctccctgtatga 1679
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 Db 1633 atctgtacccccaccctatcttaacaccacccttggtcctccactccagctccctgtatga 1692
 QY 1680 tataacctgtcaggctggctggttactggttactgaggcagagatagggaaatcctta 1739
 |||||
 Db 1693 tataacctgtcaggctggctggttactggttactgaggcagagatagggaaatcctta 1752
 QY 1740 ttaaacataacatgaatatgtgtgttttctcattgtgcaaatttaaatgaagatataat 1799
 |||||
 Db 1753 ttaaacataacatgaatatgtgtgttttctcattgtgcaaatttaaatgaagatataat 1812
 QY 1800 gtttgtatgaaaaa 1813
 |||||
 Db 1813 gtttgtatgaaaaa 1826
 |||||
 RESULT 13
 AAZ65278
 ID AAZ65278 standard; DNA; 1932 BP.
 AC AAZ65278;
 XX 23-MAR-2000 (first entry)
 DT
 DE Human secreted protein gene 29.
 KW Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;

KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KW therapy; ds.
 XX
 OS Homo sapiens.
 XX
 PD 18-NOV-1999.
 XX
 PN WO958660-A1.
 PF 06-MAY-1999; 99WO-US09847.
 XX
 PR 12-MAY-1998; 98US-0085093.
 PR 12-MAY-1998; 98US-0085094.
 PR 12-MAY-1998; 98US-0085105.
 PR 12-MAY-1998; 98US-0085180.
 PR 18-MAY-1998; 98US-0085906.
 PR 18-MAY-1998; 98US-0085920.
 PR 18-MAY-1998; 98US-0085921.
 PR 18-MAY-1998; 98US-0085922.
 PR 18-MAY-1998; 98US-0085923.
 PR 18-MAY-1998; 98US-0085924.
 PR 18-MAY-1998; 98US-0085928.
 PR 18-MAY-1998; 98US-0085925.
 PR 18-MAY-1998; 98US-0085927.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
 PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR;
 PI Lafleur DW, Endress GA, Ebner R;
 PI
 XX
 DR WPI: 2000-062296/05.
 DR P-PSDB; AAY76152.
 XX
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders -
 XX
 PS Claim 1; Page 313-314; 475pp; English.
 XX
 CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
 CC AAY76124 to AAY76223 represent the secreted proteins encoded by the 97
 CC human genes. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions,
 CC e.g. by protein or gene therapy. Also pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new genes. Specific
 CC uses are described for each of the 97 genes, based on which tissues they
 CC are most highly expressed in, and include developing products for the
 CC diagnosis or treatment of cancer, tumours, developmental abnormalities
 CC and foetal deficiencies, blood disorders, diseases of the immune system,
 CC autoimmune diseases, inflammation, allergies, asthma, psoriasis and cognitive
 CC disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin
 CC disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney
 CC disorders, digestive/endocrine disorders, infections and AIDS. The
 CC polypeptides are also useful for identifying their binding partners.

Db 1567 ctccaccaagatgaggggcagagactccagtcacgtgagtcctcccaaggcccccctgatct 1626
Qy 1624 gtaccaccacctatcaaccaccaccttggtcccaactccagtcacctgtattgatata 1683
Db 1627 gtaccaccacctatcaaccaccaccttggtcccaactccagtcacctgtattgatata 1686
Qy 1684 acctgtcaggtcgtctgtgtttagtttactcgtgggcagagatagggaattcttattaa 1743
Db 1687 acctgtcaggtcgtctgtgtttagtttactcgtgggcagagatagggaattcttattaa 1746
Qy 1744 aactaacatgaataatgtgtgttttcatttcgaatttaataagaatacataatgttt 1803
Db 1747 aactaacatgaataatgtgtgttttcatttcgaatttaataagaatacataatgttt 1806
Qy 1804 gtatgaaaaa 1813
Db 1807 gtatgaaaaa 1816

RESULT 14
AAC85076
ID AAC85076 standard; DNA; 1831 BP.
XX
AC AAC85076;
XX
DT 08-MAY-2001 (first entry)
XX
DE Atherosclerosis-associated gene seq ID No. 12.
XX
KW Atherosclerosis-associated gene; stroke; myocardial infarction; human;
KW ischemia; coronary artery disease; angina pectoris; hypertension;
KW peripheral vascular disease; renal artery stenosis; antiatherosclerotic;
KW cerebroprotective; cardiact; gene therapy; hypotensive; vasotropic;
KW antianginal; ds.
XX
OS Homo sapiens.
XX
PN WO200104264-A2.
XX
PD 18-JAN-2001.
XX
PF 28-JUN-2000; 2000WO-US17887.
XX
PR 07-JUL-1999; 99US-0349015.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Jones KA, Volkmuth W, Walker MG;
XX
DR WPI; 2001-138330/14.
XX
PT Composition comprising atherosclerosis-associated polynucleotide useful
PT in diagnosis, prognosis, treatment, and prevention of atherosclerosis
PT and stroke, myocardial infarction, or hypertension -
XX
PS Claim 1; Page 43; 58pp; English.
XX
CC The invention provides novel atherosclerosis-associated polynucleotides

CC and polypeptides encoded by the genes. Expression vectors and host cells
CC for producing the polypeptides are disclosed and methods for screening
CC or
CC purifying ligands which specifically bind to the polypeptides are also
CC provided. The polynucleotides are useful for treating diseases
associated
CC with the altered expression of a gene that is coexpressed with one or
CC more known atherosclerosis-associated genes in a subject. They are
CC useful in diagnosis, prognosis, treatment, prevention, selection and
CC evaluation of therapies for atherosclerosis including stroke, myocardial
CC infarction, transient cerebral ischemia, mesenteric ischemia, coronary
CC artery disease, angina pectoris, peripheral vascular disease, renal
CC artery stenosis, and hypertension. Sequences AAC85065-85098 represent
CC atherosclerosis-associated genes of the invention.
XX
SQ Sequence 1831 BP; 370 A; 561 C; 494 G; 406 T; 0 other;

Query Match 97.1%; Score 1760.4; DB 22; Length 1831;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1807; Conservative 0; Mismatches 6; Indels 13; Gaps 3;

Qy 1 ggagccgcccctgggtgtcagcggctcggctcccgcgacgctccggccgtcggcagcct 60
Db 3 ggagccgcccctgggtgtcagcggctcggctcccgcgacgctccggccgtcggcagcct 62
Qy 61 cggcacctgcaggtccgt-gcgtcccgcggt-ggcgcccctgactccgtccggccagg 118
Db 63 gggcacctgcaggtccgtccgtcccgcggtccggccgcccctgactccgtccggccagg 122
Qy 119 gagggccatgatctccctccggggggcccttggtgaccactgtcgtcgtttgttccct 178
Db 123 gagggccatgatctccctccggggggcccttggtgaccactgtcgtcgtttgttccct 182
Qy 179 ggggctgagtcctccctcgcgccccctcgcgggcccagctgcaactgcaactgcccgcga 238
Db 183 ggggctgagtcctccctcgcgccccctcgcgggcccagctgcaactgcaactgcccgcga 242
Qy 239 ccggtgcaggcgggtgaggaggaggagtggtcctccagcgtgtacacttgacactgcacgg 298
Db 243 ccggtgcaggcgggtgaggaggaggagtggtcctccagcgtgtacacttgacactgcacgg 302
Qy 299 ggaagtgtctcatcccaagcagtggaagtgcccttgtgatgtgttcttcaaacgaa 358
Db 303 ggaagtgtctcatcccaagcagtggaagtgcccttgtgatgtgttcttcaaacgaa 362
Qy 359 agaaaggagatcaggtgtgtcctacatcaatgggggtcacaacaaggcaaacctggagt 418
Db 363 agaaaggagatcaggtgtgtcctacatcaatgggggtcacaacaaggcaaacctggagt 422
Qy 419 atcctgtgtactcatcctcctcccggaactgtccctcgtcgggtgagggtctccagga 478
Db 423 atcctgtgtactcatcctcctcccggaactgtccctcgtcgggtgagggtctccagga 482
Qy 479 gaaagacttggccctacagctgtccgtgaatgtgcaagaacaacaaggcaaatctag 538
Db 483 gaaagacttggccctacagctgtccgtgaatgtgcaagaacaacaaggcaaatctag 542

QY 539 gggccacagcatcaaaacctagaactcaatgtaactggttccctccagctccctccatctcg 598
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Db 543 gggccacagcatcaaaacctagaactcaatgtaactggttccctccagctccctccatctcg 602
QY 599 ccgtctccagaggtgtgtcccatgttg99ggcaaacgtgacctgaagctgcagctcccaag 658
|||||
Db 603 ccgtctccagaggtgtgtcccatgttg99ggcaaacgtgacctgaagctgcagctcccaag 662
QY 659 gagtaagcccgctgttcccaataacagtgggatcgcgacagcttccatccctccagacttctt 718
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Db 663 gagtaagcccgctgttcccaataacagtgggatcgcgacagcttccatccctccagacttctt 722
QY 719 tgcacacagcatatagatgtcatccgtgggtctttaagcctcaaccaacttctgcttccat 778
|||||
Db 723 tgcacacagcatatagatgtcatccgtgggtctttaagcctcaaccaacttctgcttccat 782
QY 779 ggcctgagtcatagtctgcaaggcccaacaatgagtgggacatgcccacatgtaatgtgac 838
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Db 783 ggcctgagtcatagtctgcaaggcccaacaatgagtgggacatgcccacatgtaatgtgac 842
QY 839 gctggaagtgaagcaaca-----gggcctggaagctgacatggtctgctggaagctgtt 887
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Db 843 gctggaagtgaagcaacaggtcagtgaggggcttggaagctgacatggtctgctggaagctgtt 902
QY 888 gtgggtaccccggttggactgggtgtgtgctggctgggctgtgctcctctgtaccacgcgcgg 947
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Db 903 gtgggtaccccggttggactgggtgtgtgctggctgggctgtgctcctctgtaccacgcgcgg 962
QY 948 ggcaaggccctggaggaagcccgacaaatgatacaaggagagtgccatgtctcccgagcc 1007
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Db 963 ggcaaggccctggaggaagcccgacaaatgatacaaggagagtgccatgtctcccgagcc 1022
QY 1008 ctgacctggcccaagagctcagacacaatctccaagaatgggaccttctctgtcaccc 1067
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Db 1023 ctgacctggcccaagagctcagacacaatctccaagaatgggaccttctctgtcaccc 1082
QY 1068 tccgcagagagccctccggccaaccccatgcccctccagcctgtgtgcatgtgacccccacg 1127
|||||
Db 1083 tccgcagagagccctccggccaaccccatgcccctccagcctgtgtgcatgtgacccccacg 1142
QY 1128 cccagctctccagccaagccctgcccctcacaagaactgcccacgacagatggggccac 1187
|||||
Db 1143 cccagctctccagccaagccctgcccctcacaagaactgcccacgacagatggggccac 1202
QY 1188 cctcaaccaatatcccccatccctgtggggttctctcctctgacctgagcccgcatgggt 1247
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Db 1203 cctcaaccaatatcccccatccctgtggggttctctcctctgacctgagcccgcatgggt 1262
QY 1248 gctgtgctgtgatagtgtgctgtccagagtcgaagctggtctctggtatgatagccccac 1307
|||||
Db 1263 gctgtgctgtgatagtgtgctgtccagagtcgaagctggtctctggtatgatagccccac 1322
QY 1308 cactcatggctaaaggatgtggggtctctcctctctataagggtcacctctagcacaga 1367
|||||
Db 1323 cactcatggctaaaggatgtggggtctctcctctctataagggtcacctctagcacaga 1382
QY 1368 ggccgtgagtcatgggaaagatcacactcctgacccctagtaactgtgccccacactctct 1427
|||||

Db 1383 ggcttgatcatgggaaagagtcaacactctcgaccttagtaactctgccccacactctct 1442
QY 1428 ttactgtgggaaaaccatctcagtaagacctaaagtgtccaaggagacagaagagaagg 1487
|||||
Db 1443 ttactgtgggaaaaccatctcagtaagacctaaagtgtccaaggagacagaagagaagg 1502
QY 1488 aagtgtatctggaatgggagagacctcacaccaccctgactcctccttatgaagccag 1547
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Db 1503 aagtgtatctggaatgggagagacctcacaccaccctgactcctccttatgaagccag 1562
QY 1548 ctgtgtaaatagctactcaccaagagtgaaggggcagagactccagtaactgactcctc 1607
|||||
Db 1563 ctgtgtaaatagctactcaccaagagtgaaggggcagagactccagtaactgactcctc 1622
QY 1608 caggccctctgactgttaccccaaccctatcaaccacaccccttggtccctccactccagc 1667
|||||
Db 1623 caggccctctgactgtgtaccccaaccctatcaaccacaccccttggtccctccactccagc 1682
QY 1668 tcctgtatctatataacctgtcagagctggcttggttaggtttactggggcagagata 1727
|||||
Db 1683 tcctgtatctatataacctgtcagagctggcttggttaggtttactggggcagagata 1742
QY 1728 gggaatctctatataaacaacatgaatatgtgtgttccattgtgcaatttaata 1787
|||||
Db 1743 gggaatctctatataaacaacatgaatatgtgtgttccattgttccattgtgcaatttaata 1802
QY 1788 aagatacataatgttctgtatgaaaaa 1813
|||||
Db 1803 aagatacataatgttctgtatgagata 1828

RESULT 15
AAFA4978
ID AAFA4978 standard; cDNA; 1869 BP.
XX
AC AAFA4978;
XX
DT 28-MAR-2001 (first entry)
XX
DE Human INTERCEPT 258 coding sequence SEQ ID NO: 26.
XX
KW Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;
KW INTERCEPT 258; coronary disorder; olfactory disorder;
KW neurological disorder; pulmonary disorder; immunological disorder;
KW developmental disorder; kidney disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200078808-A1.
XX
PD 28-DEC-2000.
XX
PF 19-JUN-2000; 2000WO-US16883.
XX
PR 18-JUN-1999; 99US-0336536.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX

Db 1348 taaaggatttggggtctctctccttccctataagggtcaccctcagcacagagggcctgaagtca 1407

QY 1379 tgggaaagagtcacactcctgaaccttagtactctgccccacactctcttactgtggga 1438
 |||||

Db 1408 tgggaaagagtcacactcctgaaccttagtactctgccccacactctcttactgtggga 1467
 |||||

QY 1439 aaaccatctcagtaagacctaaagtgtccaggagacagaggaaggaagtgtgactctg 1498
 |||||

Db 1468 aaaccatctcagtaagacctaaagtgtccaggagacagaggaaggaagtgtgactctg 1527
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QY 1499 gaattgggaaggacctccaccacccctgactcctcctatgaagccagctgtgaaatc 1558
 |||||

Db 1528 gaattgggaaggacctccaccacccctgactcctcctatgaagccagctgtgaaatc 1587
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QY 1559 agctactcaccaagagtgaaggggcagagactccagtcacgtgactcctccagggccctt 1618
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Db 1588 agctactcaccaagagtgaaggggcagagactccagtcacgtgactcctccagggccctt 1647
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QY 1619 gatctgtacccccccctatctaaccacaccccttgctcccaactccagctccctgtatcg 1678
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Db 1648 gatctgtacccccccctatctaaccacaccccttgctcccaactccagctccctgtatcg 1707
 |||||

QY 1679 atataacctgtcaggtgctgtgttagtttactcggggcagagatagggaatctctt 1738
 |||||

Db 1708 atataacctgtcaggtgctgtgttagtttactcggggcagagatagggaatctctt 1767
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QY 1739 attaaaactaacatgaatatgtgtgtttcatttgcgaatttaataagatacataa 1798
 |||||

Db 1768 attaaaactaacatgaatatgtgtgtttcatttgcgaatttaataagatacataa 1827
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QY 1799 tgttctgtatgaaaaa 1813
 |||||

Db 1828 tgttctgtatgagata 1842
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Search completed: August 19, 2002, 16:16:06
 Job time: 4314 sec

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:02:47 ; Search time 54.72 Seconds
(without alignments)
8138.405 Million cell updates/sec

Title: US-09-902-759-38

Perfect score: 1813

Sequence: 1 ggaagccgcctcgggtgcag.....cataatgtttgatgaaaa 1813

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*

Result No.	Score	Query Match	Length	DB ID	Description
1	1376	75.9	1387	2	US-08-979-424-2
2	51.4	2.8	7218	1	US-08-232-463-14
3	45.4	2.5	1584	4	US-08-928-383B-1
4	45.4	2.5	2434	4	US-09-272-496-1
5	44.2	2.4	4403765	4	US-09-103-840A-2
6	43.4	2.4	4403765	4	US-09-103-840A-2
7	42.4	2.3	1095	4	US-08-928-383B-3
8	42.2	2.3	2830	1	US-07-882-292-1
9	42.2	2.3	2830	2	US-08-331-644-1
10	42.2	2.3	2830	5	PCT-US93-04102-1
11	41.8	2.3	477	4	US-09-135-994-1
12	41.6	2.3	1515	4	US-08-928-383B-25

C 13	41.2	2.3	1280	4	US-09-060-756-4	Sequence 4, Appli
14	41	2.3	4411529	4	US-09-103-840A-1	Sequence 1, Appli
15	40.4	2.2	1355	3	US-08-415-655-14	Sequence 14, Appli
C 16	37.8	2.1	2576	1	US-08-471-033-35	Sequence 35, Appli
C 17	37.8	2.1	2576	2	US-08-471-044-35	Sequence 35, Appli
C 18	37.8	2.1	2576	2	US-08-463-483A-35	Sequence 35, Appli
C 19	37.8	2.1	2576	2	US-08-471-046A-35	Sequence 35, Appli
C 20	37.8	2.1	2576	2	US-08-470-566B-35	Sequence 35, Appli
C 21	37.8	2.1	2576	2	US-08-469-334-35	Sequence 35, Appli
C 22	37.8	2.1	2576	3	US-09-300-529-35	Sequence 35, Appli
C 23	37.8	2.1	2655	1	US-08-471-033-17	Sequence 17, Appli
C 24	37.8	2.1	2655	1	US-08-471-033-26	Sequence 26, Appli
C 25	37.8	2.1	2655	2	US-08-471-044-17	Sequence 17, Appli
C 26	37.8	2.1	2655	2	US-08-471-044-26	Sequence 26, Appli
C 27	37.8	2.1	2655	2	US-08-463-483A-17	Sequence 17, Appli
C 28	37.8	2.1	2655	2	US-08-463-483A-26	Sequence 26, Appli
C 29	37.8	2.1	2655	2	US-08-471-046A-17	Sequence 17, Appli
C 30	37.8	2.1	2655	2	US-08-471-046A-26	Sequence 26, Appli
C 31	37.8	2.1	2655	2	US-08-470-566B-17	Sequence 17, Appli
C 32	37.8	2.1	2655	2	US-08-470-566B-26	Sequence 26, Appli
C 33	37.8	2.1	2655	2	US-08-469-334-17	Sequence 17, Appli
C 34	37.8	2.1	2655	2	US-08-469-334-26	Sequence 26, Appli
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C 36	37.8	2.1	2655	3	US-09-300-529-26	Sequence 26, Appli
C 37	37.8	2.1	4031	1	US-08-471-033-49	Sequence 49, Appli
C 38	37.8	2.1	4031	2	US-08-471-044-49	Sequence 49, Appli
C 39	37.8	2.1	4031	2	US-08-463-483A-49	Sequence 49, Appli
C 40	37.8	2.1	4031	2	US-08-471-046A-49	Sequence 49, Appli
C 41	37.8	2.1	4031	2	US-08-470-566B-49	Sequence 49, Appli
C 42	37.8	2.1	4031	2	US-08-469-334-49	Sequence 49, Appli
C 43	37.8	2.1	4031	3	US-09-300-529-49	Sequence 49, Appli
C 44	37.4	2.1	320	4	US-09-165-264-7	Sequence 7, Appli
C 45	37	2.0	1682	4	US-09-318-443-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-08-979-424-2

; Sequence 2, Application US/08979424

; Patent No. 5942606

; GENERAL INFORMATION:

; APPLICANT: Lal, Preeti

; APPLICANT: Corley, Neil C.

; TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Dr.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,424
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0405 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGRET03
CLONE: 1232054
US-08-979-424-2

Query Match 75.9%; Score 1376; DB 2; Length 1387;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1387; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:00:57 ; Search time 1589.67 Seconds
(without alignments)
15393.119 Million cell updates/sec

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Perfect score: 1813

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estp1:*
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8: em_hic:*
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12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vtc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB ID	Description
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C 2	1005.6	55.5	1017	9	AL547358

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C	4	947.6	52.3	986	9	AL573030	AL573030	AL573030
	5	947.6	52.3	1013	9	AL550211	AL550211	AL550211
	6	942.6	52.0	1003	9	AL552901	AL552901	AL552901
C	7	942	52.0	955	9	AL571713	AL571713	AL571713
C	8	937.2	51.7	1026	9	AL573957	AL573957	AL573957
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muscu	21	843.6	46.5	1816	11	AK009223	AK009223	Mus
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ALIGNMENTS

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prime, mRNA sequence.
ACCESSION AL573851
VERSION AL573851.1 GI:12933489
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1069)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 248 a 269 c 327 g 224 t 1 others
ORIGIN

Query Match 56.6%; Score 1026.2; DB 9; Length 1069;
Best Local Similarity 99.5%; Pred. No. 2.7e-232;
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DEFINITION AL547358 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI007YN05 5
prime, mRNA sequence.
ACCESSION AL547358
VERSION AL547358.1 GI:12881364
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1017)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 185 a 311 c 305 g 215 t 1 others
ORIGIN

Query Match 55.5%; Score 1005.6; DB 9; Length 1017;
Best local Similarity 99.8%; Pred. No. 2e-227;
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RESULT 3
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 prime, mRNA sequence.
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 VERSION AL513572.1 GI:12777066
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1045)
 AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 196 a 304 c 302 g 229 t 14 others
 ORIGIN

Query Match 54.7%; Score 992.4; DB 9; Length 1045;
 Best Local Similarity 97.0%; Pred. No. 2,7e-224;
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 SOURCE human.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 986)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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 was primed with a NotI-oligo(dT) primer. Five prime end
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 cloned into the NotI and EcoRV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 212 a 250 c 302 g 210 t 12 others
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Query Match 52.3%; Score 947.6; DB 9; Length 986;
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1013)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
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 prime, mRNA sequence.
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 SOURCE human.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1003)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 183 a 304 c 301 g 213 t 2 others
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 Db 958 ATGATATCAAGAGATGC 976

RESULT 7
 AL571713/c
 LOCUS AL571713 955 bp mRNA linear EST
 16-FEB-2001
 DEFINITION AL571713 LTI_NFL006_PL2 Homo sapiens CDNA clone CSODI031Y109 3
 prime, mRNA sequence.
 AL571713
 ACCESSION AL571713
 VERSION AL571713.1 GI:12929283
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 REFERENCE 1 (bases 1 to 955)
 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length CDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 207 a 247 c 300 g 200 t 1 others
 ORIGIN

Query Match 52.0%; Score 942; DB 9; Length 955;
 Best Local Similarity 99.7%; Pred. No. 2.3e-212;
 Matches 953; Conservative 1; Mismatches 1; Indels 1; Gaps

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 QY 858 cctgagctgcagtggtgtgtcgtgagctgtgtgtgtacccctggttgagctgggtgtgctg 917
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 Db 896 CTTGAGACTGcAGTGGTGTCTGAGACTGTGTGGTAACCTTGTTGACTGGGGTTGCTG 837
 QY 918 gctggctggtcctctgtaccacgcggggcaagggccctggagagagccagccaatgat 977
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 Db 836 GCTGGCTGGrCTCTGTATACACCGCGGGAAGGCCCTTGAGAGAGCCAGCCAATGAT 777
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 Db 776 ATCAAGAGAGATGCCATGTGCTCCCGGACCTGCGCCCAAGAGCTCAGACACATC 717
 QY 1038 tccaagaatgggaaccttctctgtcaactccgacgagccctccggccaaccatgac 1097
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 Db 716 TCCAAGATGGAGCCCTTCTCTGTACCTTCGACAGAGCCTCGGCGCACCCATGGC 657
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 QY 1218 gttctctctggtcttgagccgcatgggtgctgctgtgatggtgctgcccagagt 1277
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 Db 476 CAAGCTGCTCTCTGTATGATGACCCACCACTAATTGGCTAAAGATTGGGGTCTCT 417
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 Db 416 CTTCTATAGGGGTCACTTATGACAGAGGCTGATGAGGAAGATCACACTCC 357
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 Db 296 TAAGTGTCCAGAGACAGAAAGAGAAAGAGAGTGTGATCTGGAATTGGAGAGACCTCCA 237
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 Db 236 CCCACCCTGACTCTCTTATGAAGCCAGCTGTGAATTAAGTACTACCAAGAGTGA 177
 QY 1578 ggggacagagactccagtcactgagctcccaagcccttgatctgtaccaccaacctca 1637
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 Db 176 GGGGAGAGACTTCAGTCACTGAGTCTCCAGGCCCCCTTGATCTGTATACCCACCCCTA 117

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 QY 1771 atttgcgaatttaa 1784
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 Db 14 ATTGGCAATTAA 1
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 RESULT 9
 AL548482 969 bp mRNA linear EST
 LOCUS AL548482 16-FEB-2001
 DEFINITION AL548482 LTI_NFL006_PL2 Homo sapiens cDNA clone CSOD1014YD08 5
 prime, mRNA Sequence.
 ACCESSION AL548482
 VERSION AL548482.1 GI:12883529
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 969)
 AUTHORS Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
 source location/Qualifiers
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 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 177 a 289 c 293 g 208 t 2 others
 ORIGIN

Query Match 50.3%, Score 911.6, DB 9, Length 969;
 Best Local Similarity 98.6%, Pred. No. 3.7e-205;
 Matches 960; Conservative 2; Mismatches 7; Indels 5; Gaps

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 Db 360 CAGGTGTTGTCTTACATCATATGAGGGGTCAACAACAACTGGAGTATCTTGGTCTAC 419
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 QY 432 tccatgccccccggaacctgtccctcgcgctggaagggtctccaggaagaagactcggc 491
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 QY 492 ccctacagctgtctcgtgatatgtgcaagacaagaaggaacttagggccacagcattc 551
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QY 852 acaggcgctggagctgcagtcggtctgtctggagctgtgtgtggttacctgtgtgactgggg 911
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 QY 972 aatgatatacaagga 985
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 Db 956 AATGATATHAAGGA 969

RESULT 10
 AL549789
 LOCUS AL549789 1109 bp mRNA linear EST
 16-FEB-2001
 DEFINITION AL549789 LTI_NFL006_PL2 Homo sapiens cDNA clone CSOD1054Y101 5
 prime, mRNA sequence.
 ACCESSION AL549789
 VERSION AL549789.1 GI:12886119
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1109)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 204 a 337 c 327 g 238 t 3 others
 ORIGIN

Query Match 50.2%; Score 911; DB 9; Length 1109;
 Best Local Similarity 98.9%; Pred. No. 5.4e-205;
 Matches 937; Conservative 1; Mismatches 6; Indels 3; Gaps

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 QY 190 cccctcgccccctcgcgggccagctgcaactgcaactgtgccgccaacccgttcgag 249
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 Db 180 CCCTCGGCGCCCCCTCGCGGGGCCAGCTGCACTGCACTTGCCCGCAACCGTTGCAAG 239
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 QY 370 atcagtggtgtcctacatcaatggtgtcacaaagcaaacctgtagtacctgtgtct 429
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 QY 490 gccctcacgtgtccgtgaatgtgcaagacaacaagcaaatcaggggccacagca 549
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OY 1758 atgtgtgtttc 1768
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Db 20 ATTTGTGTAT 10

RESULT 14

AL546335
LOCUS AL546335 938 bp mRNA linear EST
16-FEB-2001

DEFINITION AL546335 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1031Y109 5
prime, mRNA sequence.

ACCESSION AL546335
VERSION AL546335.1 GI:12879351

KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 938)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES Location/Qualifiers
source 1..938

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1031Y109"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"

/note="Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dt) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the PCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 168 a 282 c 281 g 205 t 2 others
ORIGIN

Query Match 49.4%; Score 895.8; DB 9; Length 938;
Best Local Similarity 99.0%; Pred. No. 2e-201;
Matches 930; Conservative 2; Mismatches 4; Indels 3; Gaps

OY 10 ctgggtcagcggtcgcgtcccgagcagctcggcgctcgcgagcctcgacactg 69
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Db 1 CTGGGTCTCAGCGGCTTCGGCTCCCGGCACGCTCCGGCCGTGCGCA-SCTCGGACCTG 59
OY 70 caggtccgtgcgtcccgcggtggtcgccctgaactccgtcccgccaggagggccatga 129
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Db 60 CAGGTCCGTGCGTCCCGCGGCTGCGCCCTGACTCCGTCCCGGCCAGGAGGGCCATGA 119
OY 130 ttccctcccgaggccctgtgtgacccaactgtgtcggttttgttccctggggctgagt 189
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Db 120 TTTCCCTCCCGGGGGCCCTGTGTGACCAACTTGCTGGGTTTGTCTCTGGGGCTGAGTG 179

OY 190 ccctgcgccccctcgcgggccagctgcaactgcaactgtcccgcccaacgggtgcagg 249
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Db 180 CCCTCGCGCCCCCTCGCGGGGCCAGCTGCACTGCACTTGCCCGCAACCGGTTGAGG 239

OY 250 cgttgaggaggaggagtggtgtgtccagcgtgtacaccttgcaaggagggtgtctt 309
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Db 240 CGGTGAGAGGAGGAGGAGTGTGTCTTCCAGCGTGTACACCTTGACAGGGGAGGTGTCTT 299

OY 310 catcccaagcattggaggagtgcccttgatgtgtgttctcaacagaaagaaaggagg 369
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Db 300 CATCCAGCCATGGAGAGTGCCCTTGTGTGTGTCTTCAACAGAAAGAAAGAGAGG 359

OY 370 atcagtggtgtcctacatcaatgaggggtcacaaagcaaacctgagatcctgtgtct 429
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Db 360 ATCAGGTGTGTCTTACATCATATGGGGTCAACAACCAACTGAGTATCTTGTGTCT 419

OY 430 actccatgcccctcccggaacctgtccctcggtgaggggtctccaggagaaagactctg 489
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Db 420 ACTCCATGCCCCCTCCGGAACCTGTCTCCGTGAGGGTCTCCAGAGAAAGACTCTG 479

OY 490 gccctcaagctgtccgtgaatgtgcaagacaagaaggaactctaggggccacagca 549
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Db 480 GCCCCTACAGCTGCTCGTGAATGTGCAAGACAAGCAAACTTAAGGGGCGCACAGCA 539

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Db 540 TCAAAACCTTAGAACTCAATGTAATGTGTTCCCTCCAGCTCCCTCATCTCGCCGTCCAGG 599

OY 610 gtgtgccccatgtgggggcaaacgtgacacctgagctgccagtctccaaaggagtaagcccg 669
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Db 600 GTGTGCCCATGTGGGGCAACGTCGACCTGTAGCTGCCAGTCTCCAAAGGAGTAAGCCCG 659

OY 670 cgtgccaataccagtggtgagtcggcagcttccatcctccagacttcttgcaccagcat 729
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Db 660 CTGTCCAATACAGTGGGATCGGCAGCTTCCATCTTCCAGACTTCTTGTGACACGAT 719

OY 730 tagatgtcatccgtggtgtcttaagctcaccacaaccttgcgtcttccatgctgagagct 789
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OY 790 atgtctgaagggccacaatgaggtggtggtgcaactgcccgaatgtatgtacgctggaagtga 849
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Db 780 ATGTCTGCAAGGCCCAATATGAGGTGGGACTGCCCCAATGTATGTGACGCTGGAAGTGA 839

OY 850 gcaacagggcctggagctgcagtggtgtctgagagctgtgtggtaccctgtgtgactgg 909
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Db 840 GCACAGGGCCTGAGAGCTGACAGTGTGTGAGCTGTGTGTGAGTA-CCTGTGAGACTGG 898

QY 910 ggttgctgctggcgctgctcctctctgtaccacgcccggg 948
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Db 899 GGTTCGTGCTGGGCTGGT-CTTTGTACAACGCCGGGS 936

RESULT 15
AL554790
LOCUS AL554790 999 bp mRNA linear EST
16-FEB-2001

DEFINITION AL554790 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI086YJ14 5
prime, mRNA sequence.

ACCESSION AL554790
VERSION AL554790.1 GI:12895912
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 999)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source 1..999
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODI086YJ14"
/clone_lib="LTI_NFL006_PL2"
/issue_type="placenta"
/note="Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the PCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 184 a 298 c 302 g 214 t 1 others
ORIGIN

Query Match 49.4%; Score 895.8; DB 9; Length 999;
Best Local Similarity 98.8%; Pred. No. 2.1e-201;
Matches 934; Conservative 0; Mismatches 7; Indels 4; Gaps 3;
QY 12 ggggtgcagcggtcggtcccgcgacgctccggcgtgcgacgctcgacactgca 71
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Db 1 GGGTGTACGGGCTCGGCTCCCGGACGCTCCGGCGTCCGCA-CCTCGCACCTGCA 59
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QY 72 ggtcgtgctcccgcggtcgcgccctgactcgctccggcgcaaggaggacatgatt 131
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Db 60 GGTCCGTGCTCCCGCGGCTGGCGCCCTGACTCGTCCGCGCCAGGAGGAGCCATGATT 119
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QY 132 tccctcccggggccccctggtgaccaaactgtctcggttttctcctggggctgaatgac 191
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Db 120 TCCTCCCGGGGCCCTGTGTACCAACTGTCTGGGTTTTTTTCTCTGGGCTGAGTGCC 179
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QY 192 ctgcgccccctcgcgggcccgacgtgcaactgtgcccccaaccggtgtcgagcg 251
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Db 180 CTGCGGCCCCCTCGGGGGCCCGAGCTGCAACTGTGACCTGCCCCCAACCGGTTGACAGGCG 239
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QY 252 gtggaaggagggaagtgtgtgtctccagcgtgtgtacacctgtgacggggaggtgtctca 311
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QY 312 tcccaagccatggagggtgcccccttgtgatgtgtgtcttcaaacagaagaagaaggagat 371
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Db 300 TCCACAGCATGGAGGTGCCCCCTTGTGTGTGTCTTCAACAGAAAGAAAGAGAGAT 359
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QY 372 caggtgtgtctctacatcaatggtgggtcacacaagaacacactggagratcctgtgtctac 431
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Db 360 CAGGTGTGTCTCTACATCAATGGGGTCAACAACAAGCAAACTGGAGTATCTTGGTCTAC 419
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QY 492 ccctacagctgtcgtgatatgtgcaagacaagaaggaacactagaaggccacagatc 551
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Db 480 CCTACAGCTGTCTCCGGAATGTGCAAGACAACAAGCAAACTAGGGGCCACAGATC 539
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QY 552 aaaaccttagaactcaatgtactgttctcctccagctcctccatctcgtctccaaggt 611
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Db 540 AAAACCTTAGAACTCAATGTACTGTCTCTCCAGCTCTTCATCTGCCGTCTCCAGGCT 599
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QY 612 gtcgccccatgtgggggcaaacgtgacacctgagctgacagctccaagagtaagccgct 671
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Db 600 GTGCCCATGTGGGGGCAACGTGACCTGAGCTGCAGTCTCCAAAGAGTAAGCCGCT 659
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QY 672 gtccaatcacagtggtggtcggcagcttccatccttccagacttctttgacaccagcat 731
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Db 660 GTCCAATCACAGTGGGATGGGAGCTTCATCTTCCAGACTTTCTTTGACACGACATTA 719
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QY 732 gatgtcatcgtggtctttaaagcctcaaaccttctgcttccatggtcgtgagtcctat 791
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Db 720 GATGTCACTCCGTGGGTCTTTAAGCTCAACAACCTTGTCTTCATGAGCTGAGTCTAT 779
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QY 792 gtcgtcaagggccacaatgaggtgggacctgcccacgtatgacgtggaagtgaac 851
|||||
Db 780 GTCTGCAAGGCCCAATGAGGTGGGACATGCCAAATGTAATGTGACGTGAAAGTAGC 839
|||||

QY 852 acagggcctgtagctgtagtgtgtctgtagcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 911
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Db 899 TTGCTGCTGGGCTGTGTC--TCTTGTACACCCCGGGGCAAGGCC 941
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Search completed: August 19, 2002, 15:31:47
Job time: 1850 sec

ALIGNMENTS

RESULT 1

CXAR_MOUSE

ID CXAR_MOUSE STANDARD; PRT; 365 AA.
AC P97792; O09052;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cocksackievirus and adenovirus receptor homolog precursor (mCAR).
GN CXADR OR CAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=97190109; PubMed=9036860;
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Cocksackie B viruses and
RT adenoviruses 2 and 5.";
RL Science 275:1320-1323(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/MAI;
RX MEDLINE=97250541; PubMed=9096397;
RA Tomko R.P., Xu R., Philipson L.;
RT "HCAR and MCAR: the human and mouse cellular receptors for subgroup C
RT adenoviruses and group B coxsackieviruses.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Bergelson J.M., Krithivas A., Crowell T.L., Finberg R.W.;
RT "The murine CAR homologue (mCAR) is a receptor for coxsackie B
RT viruses and adenoviruses.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL; Y10320; CAA71368.1; -.
DR EMBL; U90715; AAC53148.1; -.
DR EMBL; Y11929; CAA72679.1; -.
DR MGD; MGI:1201679; Cxadr.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00410; IG_like; 1.


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DR    SMART; SM00408; IGc2; 1.
KW    Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW    Repeat.
FT    SIGNAL          1      19      POTENTIAL.
FT    CHAIN           20     365     COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR
FT                                     HOMOLOG.
FT    DOMAIN          20     237     EXTRACELLULAR (POTENTIAL).
FT    TRANSMEM        238     258     POTENTIAL.
FT    DOMAIN          259     365     CYTOPLASMIC (POTENTIAL).
FT    DOMAIN          34     127     IG-LIKE C2-TYPE DOMAIN 1.
FT    DOMAIN          155     219     IG-LIKE C2-TYPE DOMAIN 2.
FT    DISULFID        41     120     BY SIMILARITY.
FT    DISULFID        162     212     BY SIMILARITY.
FT    CARBOHYD        106     106     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT    CARBOHYD        201     201     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT    CONFLICT        340     365     VAAPNLSRMGAVPVMIPAQSKDGSIV -> FKYAYKTDGIT
FT                                     VV (IN REF. 2 AND 3).
SQ    SEQUENCE        365 AA;  39947 MW;  5445B4B52A34B2A2 CRC64;

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Query Match          17.6%;  Score 353.5;  DB 1;  Length 365;
Best Local Similarity 27.8%;  Pred. No. 1.8e-16;
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Qy     68 VPFVMWFFKQKEKE--DQVLSYINGVTTSKPGVSLVY-----SMPSRNL 109
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Db    158 FKLKCEPKEGSLPLQFEW-QKLSDSQTMPTPWLAEMTSPVISVKNASSEYSGTYSCTVQN 216

Qy    229 EVGTAQCNTLE-VSTGPGAADVAGAVVGTLLVGLGLLAGLVLLYHRR---GKALEEPAND 284
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Db    217 RVGSDQCMLRLDVPPSNRAGTIAGAVIGTLLALVLIGAILFCCHRKRREEKYEKEVHHD 276

Qy    285 IKEDAIAPRTLPPWKSSDTISKNGTLSSSVTSARALRPPHGP RP GALTPTPSLSSQALPS 344
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Db    277 IRED-----VPPPKSRTSTARSYIGSNHSSL-----GSMSPSNMEGYSKTQY 318

Qy    345 PRLPTTDGAH-PQPISPIPGGVSSSGLSRMGAVPVMVPAQSQAQSLV 390
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Db    319 NQVPSEDFERAPQSPTLAPAKVAAPNLSRMGAVPVMIPAQSKDGSIV 365

```

RESULT 2

CXAR_HUMAN

ID CXAR_HUMAN STANDARD; PRT; 365 AA.

AC P78310; O00694;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Coxsackievirus and adenovirus receptor precursor (Coxsackievirus B-
DE adenovirus receptor) (hCAR) (CVB3 binding protein).

GN CXADR OR CAR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97190109; PubMed=9036860;

RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;

RT "Isolation of a common receptor for Coxsackie B viruses and
RT adenoviruses 2 and 5.";

RL Science 275:1320-1323(1997).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97250541; PubMed=9096397;

RA Tomko R.P., Xu R., Philipson L.;

RT "hCAR and mCAR: the human and mouse cellular receptors for subgroup C
RT adenoviruses and group B coxsackieviruses.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=20008750; PubMed=10543405;

RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human
RT Coxsackievirus B-adenovirus receptor gene.";

RL Hum. Genet. 105:354-359(1999).

RN [4]

RP SEQUENCE FROM N.A.

RA Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;

RT "Sequence and expression of CXADR, the human gene for the
RT coxsackievirus and adenovirus receptor.";

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND
CC SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

CC -----

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CC -----

DR EMBL; Y07593; CAA68868.1; -.

DR EMBL; U90716; AAC51234.1; -.

DR EMBL; AF169366; AAF05908.1; -.

DR EMBL; AF169360; AAF05908.1; JOINED.

DR EMBL; AF169361; AAF05908.1; JOINED.
 DR EMBL; AF169362; AAF05908.1; JOINED.
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 DR EMBL; AF169364; AAF05908.1; JOINED.
 DR EMBL; AF169365; AAF05908.1; JOINED.
 DR EMBL; AF200465; AAF24344.1; -.
 DR MIM; 602621; -.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00410; IG_like; 1.
 DR SMART; SM00408; IGc2; 1.
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 365 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
 FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 258 POTENTIAL.
 FT DOMAIN 259 365 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 34 127 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 155 219 IG-LIKE C2-TYPE DOMAIN 2.
 FT DISULFID 41 120 BY SIMILARITY.
 FT DISULFID 162 212 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 365 AA; 40029 MW; AB01C6346CB7FE64 CRC64;

Query Match 17.0%; Score 343; DB 1; Length 365;
 Best Local Similarity 27.5%; Pred. No. 9e-16;
 Matches 106; Conservative 67; Mismatches 147; Indels 66; Gaps 14;

Qy 31 LQLHL PANRLQAVEGGEVVLPAWYTLHGEVSSSQPWEVPFVMWFFK--QKEKEDQVLSYI 88
 | : | : : | | : | | : : | : | : | :
 Db 20 LSITTPEEMIEKAKGETAYLPCKFTLSPE--DQGPLDIE--WLISPADNQKVDQVIILY 74
 Qy 89 NGVTTSKPGVSLVY-----SMPSRNLSLRLEGLQEKDSGPYSCSVNVQD 132
 : | : | : : | : | : | : | : | : | :
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 Db 241 GAIIGTLLALALI-GLIIFCCRKKRREEKEYEKEVHHDIRE-----VPPPKSRTSTARS 293
 Qy 308 GTLSSVTSARALRPPH--GPPRPGALTPTPSLSSQALP-SPRLPTTDGAHPQPISPIPGG 364
 | : : | : : | : : | : : | : : | : : | : : | : :
 Db 294 YIGSNHSSLGSMSPSNMEGYSKT-QYNQVPSEDFERTPQSPTLP-----PAK 339
 Qy 365 VSSGSLSRMGAVPVMVPAQSQAGSLV 390
 | : : | | | | | : | | | : | | | : | | : | :
 Db 340 VAAPNLSRMGAIPVMIPAQSKDGSIV 365